

OM protein - protein search, using Bw model
Run on: February 16, 2006, 16:57:42 ; Search time 186 Seconds
(without alignments)
Scoring table: BLOSUM62
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1980b:*

2: geneseqp1990b:*

3: geneseqp2000b:*

4: geneseqp2001b:*

5: geneseqp2002b:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004bs:*

9: geneseqp2005b:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 18 derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2059	100.0	400	AAY03098 Bovine sc
2	1381	67.1	349	AAR05508 Scavenger
3	1381	67.1	453	AAR05509 Scavenger
4	1381	67.1	453	AAR27036 Bovine sc
5	1047.5	50.9	451	AJW19708 Macrophag
6	1046.5	50.8	451	Adi62129 Human mac
7	1042.5	50.6	358	AAR21513 Human sca
8	1042.5	50.6	358	AAR40803 Human sca
9	1042.5	50.6	358	Akw08078 Type II m
10	1042.5	50.6	358	Abr49716 Human typ
11	1042.5	50.6	7	Abd89003 Human mac
12	1042.5	50.6	358	Adq39735 Human myo
13	1042.5	50.6	358	Adq39731 Human myo
14	1042.5	50.6	8	Adq39734 Human myo
15	1042.5	50.6	388	Adq39733 Human myo
16	1042.5	50.6	451	Adr21512 Human sca
17	1042.5	50.6	451	Aar40802 Human sca
18	1042.5	50.6	451	Aaw0877 Type I ma
19	1042.5	50.6	451	Aab00080 Protein o
20	1042.5	50.6	451	Aab49715 Human typ
21	1042.5	50.6	451	Adi62127 Human mac
22	1042.5	50.6	451	Adi62123 Human mac
23	1042.5	50.6	451	Adi62125 Human mac
24	1042.5	50.6	451	Adi62126 Human mac

25	1042.5	50.6	451	8	ADL1497	Adl1497
26	1042.5	50.6	451	8	ADQ39732	Adq39732 Human myo
27	1042.5	50.6	451	8	ADR45547	Adr45547 Homologue
28	1042.5	50.6	451	8	ADP2429	Adp2429 PRO polyp
29	1042.5	50.6	451	8	ADI62128	Adi62128 Human mac
30	1040.5	50.5	451	8	ADI62130	Adi62130 Human mac
31	1039.5	50.5	451	8	ADI62131	Adi62131 Human mac
32	1034.5	50.2	451	8	ADP2035	Adp2035 Human sol
33	1032.5	50.1	451	2	ADP28571	Adp28571 Murine ma
34	801	38.9	454	7	ADP28571	Adp28571 Murine ma
35	801	38.9	458	8	ADR45545	Adr45545 Mouse typ
36	680.5	33.1	502	8	ADM97493	Adm97493 Cld1-19G-
37	678.5	33.0	581	9	ADP28082	Adp28082 Circular
38	678	32.9	128	9	ADV78149	Adv78149 Chicken i
39	678	32.9	152	2	ADM97493	Adm97493 Wild-type
40	678	32.9	152	2	ARY17867	Arg17867 Chicken a
41	678	32.9	152	8	ADP26598	Adp26598 Chicken a
42	678	32.9	152	9	AER28059	Aer28059 Chicken a
43	678	32.9	153	9	ADV78159	Adv78159 Barley am
44	678	32.9	161	3	AYA4699	Aya4699 Potato pr
45	678	32.9	269	8	ADM97489	Adm97489 Cld1-19G-
ALIGNMENTS						
RESULT 1						
RAY03098						
ID	RAY03098	standard; protein; 400 AA..				
XX						
AC	RAY03098;					
XX						
DT	03-DEC-1999	(first entry)				
XX						
DB	Bovine scavenger receptor class A (sScR)/avidin fusion protein.					
XX						
KW	Scavenger receptor class A; sScR; avidin; fusion protein; bovine; ECD; membrane-spanning domain; extracellular domain; biotin-binding activity; endocytosis.					
XX						
OS	Synthetic.					
OS	Bos taurus.					
XX						
PN	W09942577-A2.					
XX						
PD	26-APR-1999.					
XX						
PP	23-FEB-1999;	99W0-GB000546.				
XX						
PR	23-FEB-1998;	98GB-00003757.				
PR	24-JUN-1998;	98GB-00013653.				
XX						
PA	(EURO-) EUROGENE LTD.					
XX						
PI	Yla-Herttula S, Kulomaa M, Lehtolainen P, Marjomaki V, Airene K;					
XX						
PS	DR	WPI; 1999-561345/47.				
XX						
PS	DR	N-PSB; AAZ0997.				
XX						
PS	Claim 5; Page 21-23; 23pp; English.					
XX						
CC	This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (ECD), where the ECD comprises biotin-binding activity. Using the protein or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence represents a bovine scavenger receptor class A/avidin fusion protein which is used in the					

CC description of the invention
 XX • Sequence 400 AA:
 SQ Query Match 100.0%; Score 2059; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.2e-156; Mismatches 0; Indels 0; Gaps 0;
 Matches 400; Conservative 0;
 QY 1 MAQWDDPPDQOEDTSCTESVKFDARSVTALLPPHPKNGPTLQERMKSYKTTALITYLIV 60
 DB 1 MAQWDDPPDQOEDTSCTESVKFDARSVTALLPPHPKNGPTLQERMKSYKTTALITYLIV 60
 SQ 61 FVVLVPIIGIVAQQLKWEETNCTVGSVNAIDISPSEGKNGSEDEMFRBAMERMSNM 120
 DB 61 FVVLVPIIGIVAQQLKWEETNCTVGSVNAIDISPSEGKNGSEDEMFRBAMERMSNM 120
 QY 121 BSRIQVLSDNEANLDAKDNFONFSITTDORFNDVFLQNLSSQHEHNTIGDISKLV 180
 DB 121 BSRIQVLSDNEANLDAKDNFONFSITTDORFNDVFLQNLSSQHEHNTIGDISKLV 180
 QY 181 GLNTVVLQFSIETLNGRVOENAKQOBENRKLERIYNSAEIKSLDEKQVYLEQIK 240
 DB 181 GLNTVVLQFSIETLNGRVOENAKQOBENRKLERIYNSAEIKSLDEKQVYLEQIK 240
 QY 241 GEMKULNNITNDRLKDWHSQTKNITLQG 300
 DB 241 GEMKULNNITNDRLKDWHSQTKNITLQG 300
 QY 301 FGTTVITAVTSNETKESPHGTGTONTINKTOPFGFTWAKFSESTVFTGQFIDRN 360
 DB 301 FGTTVITAVTSNETKESPHGTGTONTINKTOPFGFTWAKFSESTVFTGQFIDRN 360
 QY 361 GKEVLTKMWLRSSVADGDDKATRVGINFTRUKE 400
 DB 361 GKEVLTKMWLRSSVADGDDKATRVGINFTRUKE 400

RESULT 2
 AAR05508
 ID AAR05508 standard; protein; 349 AA.
 XX AC AAR05508;
 XX DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 23-OCT-1990 (first entry)
 XX DE Scavenger receptor protein with affinity for acylated low density lipoprotein (aLDL).
 XX KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
 OS Synthetic.
 XX PN WO9005748-A.
 XX PD 31-MAY-1990.
 XX PR 15-NOV-1988; 88US-00272002.
 PR 09-AUG-1989; 89US-00391486.
 AX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Kodama, T., Krieger, M.;
 XX DR WPI; 1990-193408/25.
 DR N-PSDB; AAQ04925.
 XX PT New receptor protein - has affinity for acetylated low density lipoprotein and corresponding antibodies and DNA sequences.
 XX PT

RESULT 3
 AAR05509
 ID AAR05509 standard; protein; 453 AA.
 XX AC AAR05509;
 XX DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 23-OCT-1990 (first entry)
 XX DE Scavenger receptor protein with affinity for acylated low density lipoprotein (aLDL).
 XX KW Acylated low density lipoprotein; aLDL; atherosclerotic plaque; ds.
 OS Synthetic.
 XX PN WO9005748-A.
 XX PD 31-MAY-1990.
 XX PR 15-NOV-1988; 88US-00272002.
 PR 09-AUG-1989; 89US-00391486.
 AX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Kodama, T., Krieger, M.;
 XX DR WPI; 1990-193408/25.
 DR N-PSDB; AAQ04926.
 XX PT New receptor protein - has affinity for acetylated low density lipoprotein and corresponding antibodies and DNA sequences.
 XX PT

PS Disclosure; Page 2; 79pp; English.
 XX
 Receptor protein, and fragments and analogues thereof may be immobilised on a support and used in assay and purification of the aLDL target. Labelled Abs, raised to the protein may be injected into the vascular system to detect the presence of atherosclerotic plaques. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 CC Sequence 349 AA;
 SQ Query Match 67.1%; Score 1381; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3e-102; Mismatches 0; Indels 0; Gaps 0;
 Matches 272; Conservative 0;
 QY 1 MAQWDDPPDQOEDTSCTESVKFDARSVTALLPPHPKNGPTLQERMKSYKTTALITYLIV 60
 DB 1 MAQWDDPPDQOEDTSCTESVKFDARSVTALLPPHPKNGPTLQERMKSYKTTALITYLIV 60
 QY 61 FVVLVPIIGIVAQQLKWEETNCTVGSVNAIDISPSEGKNGSEDEMFRBAMERMSNM 120
 DB 61 FVVLVPIIGIVAQQLKWEETNCTVGSVNAIDISPSEGKNGSEDEMFRBAMERMSNM 120
 QY 121 BSRIQVLSDNEANLDAKDNFONFSITTDORFNDVFLQNLSSQHEHNTIGDISKLV 180
 DB 121 BSRIQVLSDNEANLDAKDNFONFSITTDORFNDVFLQNLSSQHEHNTIGDISKLV 180
 QY 181 GLNTVVLQFSIETLNGRVOENAKQOBENRKLERIYNSAEIKSLDEKQVYLEQIK 240
 DB 181 GLNTVVLQFSIETLNGRVOENAKQOBENRKLERIYNSAEIKSLDEKQVYLEQIK 240
 QY 241 GEMKULNNITNDRLKDWHSQTKNITLQG 300
 DB 241 GEMKULNNITNDRLKDWHSQTKNITLQG 300
 QY 301 FGTTVITAVTSNETKESPHGTGTONTINKTOPFGFTWAKFSESTVFTGQFIDRN 360
 DB 301 FGTTVITAVTSNETKESPHGTGTONTINKTOPFGFTWAKFSESTVFTGQFIDRN 360
 QY 361 GKEVLTKMWLRSSVADGDDKATRVGINFTRUKE 400
 DB 361 GKEVLTKMWLRSSVADGDDKATRVGINFTRUKE 400

PS Disclosure; Page 7; 79pp; English.

XX Receptor Protein, and fragments and analogues thereof may be immobilised

CC on a support and used in assay and purification of the aLDL target.

CC Labelled Abs, raised to the protein may be injected into the vascular

CC system to detect the presence of atherosclerotic plaques. (Updated on 31-

CC OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR

CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-

CC 2003 to correct PI field.)

XX SQ Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Indels 0; Gaps 0;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

Db 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

QY 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

Db 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

QY 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

Db 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

QY 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

Db 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

QY 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

Db 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

SQ Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Indels 0; Gaps 0;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

Db 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

QY 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

Db 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

QY 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

Db 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

QY 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

Db 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

QY 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

Db 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

SQ Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Indels 0; Gaps 0;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

Db 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

QY 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

Db 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

QY 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

Db 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

QY 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

Db 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

QY 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

Db 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

SQ Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Indels 0; Gaps 0;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

Db 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

XX 22-FEB-1991; 91US-0066227.

BR XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Krieger M;

XX WPI; 1992-315935/38.

DR N-PSDB; AJQ28540.

XX PT Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein.

PT XX Disclosure; Page 38; 56pp; English.

CC The bovine scavenger receptor protein sequence was deduced from the DNA sequence obt'd. by screening a bovine lung cDNA library with degenerate probes designed based on fragments of the purified scavenger receptor protein. The scavenger receptor protein has a binding capacity for acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments of the extracellular portion of the scavenger receptor protein inactivate endotoxin-related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports for purification purposes. The fragments may be modified to have greater binding affinity for the endotoxin-related substance than the native scavenger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols. that bind the scavenger receptor protein or of organisms which express such mols. See also AAR27035.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC Revised record issued on 23-SEP-2004 : Correction to Feature Table Key

XX SQ Sequence 453 AA;

Query Match 67.1%; Score 1381; DB 2; Length 453;

Best Local Similarity 100.0%; Pred. No. 4.3e-102; Indels 0; Gaps 0;

Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

Db 1 MAQWDDPFQDQEDTDSCTESTKFDARSVTALLPPHRKGNGPTLQERMKSYKALITLYLIV 60

QY 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

Db 61 FVVLVPIIGIVAAQLKMETKNTCTGVSNAIDSPEKGKNGSEDEMFRBAVERMNSM 120

QY 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

Db 121 ESRIQVLSDNANLDAKNAKPNFSITDQRFNDVLQFOLNSLSSIOBHENITGDISLV 180

QY 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

Db 181 GIANTTVDLQSIETINGRVOENAFAKQOEENRKLSERIYNAESAIEKSLDEKQVYLEQIK 240

QY 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

Db 241 GEMKLNNITDRLKWDWERSQTLKNTLLOG 272

XX 19-AUG-1997 (first entry)

DE Macrophage scavenger receptor protein.

XX Macrophage scavenger receptor protein; MSRP; human; lipoteichoic acid; LTA; Gram-positive bacteria; cell wall; atherosclerosis; host defence;

XX WO9214482-A1.

XX 03-SEP-1992.

XX 21-FEB-1992; 92WO-US001370.

XX	KW	septicaemia; inhibitor; complement activation; cytokine release; therapy;
XX	KW	nitric oxide production; bacterial infection; septic shock.
OS	XX	<i>Homo sapiens.</i>
PN	XX	US5624904-A.
	XX	29-APR-1997.
PD	XX	
PF	XX	17-NOV-1993; 93US-00154365.
PR	XX	17-NOV-1993; 93US-00154365.
PA	XX	(MASS) MASSACHUSETTS INST TECHNOLOGY.
PA	XX	(UTYA) UNIV YALE.
PI	XX	Krieger M, Joiner KA;
DR	XX	WPI; 1997-250236/23.
PN	XX	N-PSDB; AAT68796.
PT	XX	Treatment of septicaemia caused by Gram-positive bacteria - by administration of macrophage scavenger receptor protein.
PS	XX	Disclosure; Col 23-26; 16pp; English.
CC	XX	This sequence represents the human macrophage scavenger receptor protein (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad binding specificity for polyanionic ligands, and have been implicated in atherosclerosis and a variety of host defence functions. This protein can be used in the method of the invention. The method of the invention is for the treatment of septicaemia caused by Gram-positive bacteria. The method comprises administration of MSRP in an amount sufficient to inhibit complement activation, cytokine release or nitric oxide production induced by LTA released by the Gram-positive bacteria. In addition to treating Gram-positive septic shock, the MSRP can be used to screen for other compounds for treating Gram-positive septic shock. MSRP can also be used to purify, label or detect LTA or LTA-containing cells. MSRP, active MSRP fragment, anti-MSRP antibodies or other compounds that inhibit binding of Gram-positive bacteria to MSRP can be used to treat pathologies such as septicaemia, Gram-positive bacterial infection, Gram-positive septicemia or Gram-positive or Gram-negative septic shock.
CC	XX	Sequence 451 AA;
CC	XX	Query Match 50.9%; Score 1047.5; DB 2; Length 451; Best Local Similarity 72.5%; Pred. No. 2.7e-75; Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;
QY	1	MAQWDDPDDQDENTDCSCTESVKPDKRSVDTALLPPHPKNGPTQIERNMSKSYKTAITYLYLIV 60
DB	1	MEQWDHFFHNOQEDTDSCESEVKPDKRSVDTALLPPHPKNGPTQIERNMSKSYKTAITYLYLIV 60
QY	61	FVWVJPIVIGIVAAQQLKWTCTGVSNA-DISSPSPKGKNGSEDEMFRERWERMNSN 119
DB	61	FAVWIPPLIGIVAAQQLKWTCTGVSNSSTNANDITOSLYGKNDSEBMRFOBVFMEHMSN 120
QY	120	MESRIQYLSNEANLDAKOFQNSITDQRENDVFLQASLSSSQEHENIGIGTSKL 179
DB	121	MEKQHQHIDMEANLDAKOFQNSITDQRENDVFLQASLSSSQEHENIGIGTSKL 180
QY	180	VGLNTVLDIQLQFSTIETNGVQENAFKQQEMRKLERINMASAEIKSLDEKQVVLQEI 239
DB	181	ISLWVTLIDLQQLNTEINTLNGKIQENFTPKQOBISKLERVNTSAEIMAKEGQVHLEQI 240
QY	240	KGEMKLNNNTNDLRLKDWEHSQTLKNTLQG 272
DB	241	KGEVKVNNNTNDLRLKDWEHSQTLKNTLQG 273
PS	XX	Claim 1; Page; 21pp; English.
CC	XX	The invention describes a method of screening a subject for increased risk of prostate cancer or asthma, or decreased risk of cardiovascular disease. The method comprises: detecting the presence or absence of an MSRI mutation in the subject, and determining that the subject is at increased risk of prostate cancer, increased risk of asthma, or decreased risk of cardiovascular disease due to the presence or absence of the MSRI mutation consisting of H41R, G369S, R293X, P275A, D91Y, V113A, S41Y, P36A or I154V. The method is useful for screening a subject for increased risk of prostate cancer or asthma, or decreased risk of cardiovascular disease. This is the amino acid sequence of a human macrophage scavenger protein 1 (MSRP) mutant of the invention. Note: This sequence does not appear in the printed specification but has been created using information given in the specification.
CC	XX	Sequence 451 AA;
CC	XX	Query Match 50.8%; Score 1046.5; DB 8; Length 451; Best Local Similarity 72.5%; Pred. No. 3.3e-75; Matches 198; Conservative 41; Mismatches 33; Indels 1; Gaps 1;
QY	1	MAQWDDPDDQDENTDCSCTESVKPDKRSVDTALLPPHPKNGPTQIERNMSKSYKTAITYLYLIV 60
DB	1	MEQWDHFFHNOQEDTDSCESEVKPDKRSVDTALLPPHPKNGPTQIERNMSKSYKTAITYLYLIV 60
QY	61	FVWVJPIVIGIVAAQQLKWTCTGVSNA-DISSPSPKGKNGSEDEMFRERWERMNSN 119
DB	61	FAVWIPPLIGIVAAQQLKWTCTGVSNSSTNANDITOSLYGKNDSEBMRFOBVFMEHMSN 120

Qy	120 MERSIQQLSDNEANLIDAKNQNFSITTDQPRNDVAFOLNSLSS10BHENIGIDISKL 179 : : : : : : : : : : : : 121 MEKRICQHILDMERANLMDTEHQNFSMTDQPRNDLQLS1FSSVQGHGRNADEISKL 180	Db	181 ISLNTTILDQDQNTENINGK1QENTFKQEBISKLBRVNVSAEIMAMKBRQVHLEQI 240 : : : : : : : : : : 240 KGEMKLANTIDLRKWDENSQTLKNTLQG 272
Qy	180 VGLNTTVDLQPSIETNGRQENAFQKQEMKLERIVMASAKSLDKQVLEQI 239 : : : : : : : : : : 181 ISLNTTILDQDQNTENINGK1QENTFKQEBISKLBRVNVSAEIMAMKBRQVHLEQI 240	Db	241 KGEMKLANTIDLRKWDENSQTLKNTLQG 273
Qy	240 KGEMKLANTIDLRKWDENSQTLKNTLQG 272 : : : : : : : : 241 KGEMKLANTIDLRKWDENSQTLKNTLQG 273	RESULT 7	
Db		AAR21513	
ID	AAR21513 standard; protein; 358 AA.	XX	
AC	AAR21513;	XX	
XX		XX	
DT	25-MAR-2003 (revised)	XX	
DT	19-MAY-1992 (first entry)	XX	
XX		XX	
DE	Human scavenger receptor type II.	XX	
XX		XX	
KW	Lipoproteins.	XX	
XX		XX	
OS	Homo sapiens.	XX	
XX		XX	
PN	JP03290184-A.	XX	
XX		XX	
PD	19-DEC-1991.	XX	
XX		XX	
PP	06-APR-1990; 90JP-00090274.	XX	
XX		XX	
PR	06-APR-1990; 90JP-00090274.	XX	
XX		XX	
PA	(CHUS) CHUGAI PHARM CO LTD.	XX	
DR	WPI; 1992-051436/07.	XX	
N-PSDB	AQ021550.	XX	
XX		XX	
PT	New scavenger receptor-producing animal cells - which have been transformed with vector contg. gene for coding human scavenger receptor I	XX	
PT	or II type under control of promoter, etc.	XX	
XX		XX	
PS	Disclosure: Fig 2; 9pp; Japanese.	XX	
XX		XX	
CC	The gene encoding the receptor can be expressed from a cytomegalo- virus promoter in a host cell e.g. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified lipo- proteins or modified substances in the blood. See also AAR21512. (Updated on 25-MAR-2003 to correct PA field.)	XX	
SQ	Sequence 358 AA:	XX	
Query Match	50.6%; Score 1042.5; DB 2; Length 358;	XX	
Best Local Similarity	72.2%; Pred. No. 4.9e-75; Mismatches 34; Indels 1; Gaps 1;	XX	
Matches	197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;	XX	
Qy	1 MAQWDDDPDQEDTDCTESTKPSKDPARSTVALLPDKPGKPLQERMKSYKALITYLIV 60 : : : : : : : : : 1 MEQWDHFHQNQBDTDSCESEVKPSKDPARSTVALLPDKPGKPLQERMKSYKALITYLIV 60	Db	61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119 : : : : : : : 61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119
Qy	1 MAQWDDDPDQEDTDCTESTKPSKDPARSTVALLPDKPGKPLQERMKSYKALITYLIV 60 : : : : : : : 1 MEQWDHFHQNQBDTDSCESEVKPSKDPARSTVALLPDKPGKPLQERMKSYKALITYLIV 60	Db	61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119 : : : : : : 61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119
Qy	61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119 : : : : : 61 FVVLVLPITIGVAAQLKMKWETKNTCTVGSVNA-DISPSPEKGKNGSEDEMFRREAVMERMN 119	Db	120 MERSIQQLSDNEANLIDAKNQNFSITTDQPRNDVAFOLNSLSS10BHENIGIDISKL 179 : : : : : 121 MEKRICQHILDMERANLMDTEHQNFSMTDQPRNDLQLS1FSSVQGHGRNADEISKL 180
Qy	120 MERSIQQLSDNEANLIDAKNQNFSITTDQPRNDVAFOLNSLSS10BHENIGIDISKL 179 : : : : 121 MEKRICQHILDMERANLMDTEHQNFSMTDQPRNDLQLS1FSSVQGHGRNADEISKL 180	Db	180 VGLNTTVDLQPSIETNGRQENAFQKQEMKLERIVMASAKSLDKQVLEQI 239 : : : : 181 ISLNTTILDQDQNTENINGK1QENTFKQEBISKLBRVNVSAEIMAMKBRQVHLEQI 240
Qy	180 VGLNTTVDLQPSIETNGRQENAFQKQEMKLERIVMASAKSLDKQVLEQI 239 : : : : 181 ISLNTTILDQDQNTENINGK1QENTFKQEBISKLBRVNVSAEIMAMKBRQVHLEQI 240	Db	240 KGEMKLANTIDLRKWDENSQTLKNTLQG 272

QY	180	VGILANTVLDQFESIETANGRVQENAFQOEEENRKLIERIYASABEKSLSDEKQVYQEI	239
Db	: : : : : : : : : : : : :	240	KGEMKLANNITNDLQWHRQQTQKNTLQG 272
QY	181	ISLNTTLDLQNIENLNGKLOQNTFKQOEBSKLERVYNVSAEIMAMKKEQVHILQEI	240
Db	241	KGEVKVANNITNDLQWHSQTLRNUITLQG 273	
RESULT 12			
ADQ39735			
ID	ADQ39735	standard; protein; 358 AA.	
XX			
AC	ADQ39735;		
XX			
DT	18-NOV-2004	(first entry)	
XX			
DB	Human	myocardial infarction-associated gene derived protein, SEQ ID 1398.	
XX			
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;		
KW	cardiant; gene therapy; human.		
XX			
OS	Homo sapiens.		
XX			
RN	W02004058032-A2.		
XX			
PD	15-JUL-2004.		
XX			
PP	22-DEC-2003; 2003WO-US0409978.		
XX			
PR	20-DEC-2002; 2002US-0434778P.		
PR	10-MAR-2003; 2003US-0453135P.		
PR	30-APR-2003; 2003US-046612P.		
PR	23-SEP-2003; 2003US-050455P.		
XX			
PA	(APPL-1) APPLERA CORP.		
XX			
PT	Cargill M, Devlin JJ, Rakoubova O;		
XX			
DR	WPI; 2004-533949/51.		
XX			
N-PSDB;	ADQ38907.		
XX			
PT	Identifying an individual who has an altered risk for developing polymorphism in		
PT	myocardial infarction by detecting a single nucleotide polymorphism in		
XX	the individual's nucleic acids.		
RS	Claim 10; SEQ ID NO 1398; 145pp; English.		
XX			
CC	The invention relates to a novel method for identifying an individual who		
CC	has an altered risk for developing myocardial infarction. The method		
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of		
CC	the nucleotide sequences given in the specification in the individual's		
CC	nucleic acids, where the presence of the SNP is correlated with an		
CC	altered risk for myocardial infarction in the individual. The invention		
CC	further comprises: an isolated nucleic acid molecule comprising at least		
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in		
CC	the specification or its complement and encoding any one of the amino		
CC	acid sequences given in the specification; an isolated polypeptide		
CC	comprising an amino acid sequence given in the specification; an antibody		
CC	that specifically binds to the polypeptide or its antigen-binding		
CC	fragment; an amplified polynucleotide containing an SNP given in the		
CC	specification and which is between about 16 and 1000 nucleotides in		
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the		
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a		
CC	nucleic acid molecule; a method of detecting a variant polypeptide; and a		
CC	method for identifying an agent useful in treating or preventing		
CC	myocardial infarction. The novel detection method has cardiant activity.		
CC	The nucleic acids of the invention may be used in gene therapy. The		
CC	method is useful in identifying an individual who has an increased or		
CC	decreased risk for developing myocardial infarction and for preparing a		
CC	composition for treating or preventing myocardial infarction. This		
CC	sequenace represents the protein of a human myocardial infarction-		

CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 CC
 XX sequence 358 AA;
 SQ

Query Match	50 61;	Score 1042.5;	DB 8;	Length 358;					
Best Local Similarity	72.2%	Pred. No. 4.9e-75;							
Matches	197;	Conservative	41;	Mismatches	34;	Indels	1;	Gaps	1.
QY	1 MAQWMDPDPQDQEDTSCTESVKFDRSASVTALLPPHRKNGPTLQERNSKSYKALITYLIV	60							
Db	1 MEQWMDPDPQDQEDTSCTESVKFDRSASVTALLPPHRKNGPTLQERNSKSYKALITYLIV	60							
QY	61 FVWVLPPIGIVAAQQLKWMETKNTGTVGSNA-DISPSPEGKNGNSIDEMRFAEVMRMSN	119							
Db	61 FAVLPLIGITVAQQLKWMETKNTGTVGSNA-DISPSPEGKNGNSIDEMRFAEVMRMSN	120							
QY	120 MESSRQYLSNEANILDAKQFQNPSITDQRFNDVLFQINSLLSQIQEHENIGIJKSL	179							
Db	121 MEKROQHILDEANILDAKQFQNPSITDQRFNDVLFQINSLLSQIQEHENIGIJKSL	179							
QY	180 VGLNTTVDLQFSIETNGVQENAFQKQENRKEERIYNSAETKSLSDERKQVYQEI	239							
Db	181 ISLNNTTLDQQLNENILANGKIQENTFKQOELTSKLSERIVTIVNSAEMAKKEQVHQEI	240							
QY	240 KGEMIQLANNITNDLAKDWEHSQTQINNTLQG	272							
Db	241 KGEVVKVANNITNDLAKDWEHSQTQINNTLQG	273							

RESULT 13
 ID ADQ39731
 ADQ39731 standard; protein; 358 AA.
 AC ADQ39731;
 XX
 DT 18-Nov-2004 (first entry)
 XX Human myocardial infarction-associated gene derived protein, SEQ ID 1394.
 XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004058052-A2.
 XX
 PD 15-JUL-2004.
 XX
 PF 22-DBC-2003; 2003WO-US040978.
 PR 20-DBC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0452135P.
 PR 30-APR-2003; 2003US-046412P.
 PR 23-SEP-2003; 2003US-0504955P.
 PR
 PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin JJ,
 XX
 DR WPI; 2004-533349/51.
 DR N-PGPB; ADQ3803.
 PS
 PT Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
 CC
 PT
 PS Claim 10; SEQ ID NO 1394; 145pp; English.
 XX
 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC an electronic sequence listing downloaded from the WIPO website.
 XX sequence 358 AA;

the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk, for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is 18 an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiotonic activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 358 AA;

Query	Match	50.6%	Score	1042.5;	DB	8;	Length	358;	
Best	Local Similarity	72.2%	Pred. No.	4.9e-75;					
Matches	197;	Conservative	41;	Mismatches	34;	Indels	1;	Gaps	1;
QY	1	MAGQDDDFPQQEDTSCTCSVKFDRASVTLALLPPRKGPTLQERNSYKVALILIV	60						
Db	1	MEQDHFHFNQKQEDTSCTCSVKFDRASVTLALLPPRKGPTLQERNSYKVALILIV	60						
QY	61	FVWVMPVPIGIVAAQILKWKETNCTGVNSA-DISPPGKONGSEDEMFRRAVMEERN	119						
Db	61	FAVILPLIGIVAAQILKWKETNCTGVNSA-DISPPGKONGSEDEMFRRAVMEERN	119						
QY	120	MESIQYQSLSDNEAMULDAKRNQFNSITDORFNDLQFQNSLSSQEHENIGDQSKL	179						
Db	121	MERKIOHILDEAMULDTEHFRQNSFMTDORFNDLQFQNSLSSQEHENIGDQSKL	180						
QY	180	VGLNTVILQFSLTEIENGQVQENAKPQKOBEMRKEIRMASAKLSDKQVLEQI	239						
Db	181	ISLNTTLLQINTEENLQIQTENFKQOBELSKSERVTVNSAEMAMKSEQVHLEQEI	240						
QY	240	KGEMKLLNNTINDLRLKDWHSQTKNITLQG	272						
Db	241	KGEVVKVNNITNDLRLKDWHSQTKNITLQG	273						

RESULT 14

ID	ADQ39734	standard; protein: 358 AA.
XX	ADQ39734	
AC	ADQ39734;	
DT	18-NOV-2004 (first entry)	
DE	Human myocardial infarction-associated gene derived protein, SEQ ID 1397.	
XX		
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;	
XX	cardiant; gene therapy; human.	
OS	Homo sapiens.	
XX		
PN	WO2004058052-A2.	
XX		
PD	15-JUL-2004.	
XX		
PP	22-DEC-2003; 2003WO-US040978.	
XX		

QY 1 MAQNDDFPQOQDTSDCTESKFDARSVALLPHPKNGPTLORMSYKTLITYLIV 60
Db 1 MEQNDHFMQOQDIDSCSSESVKFDARSMALLPENPKNSLQEKLSKPAJALYLV 60
QY 61 FVVLVPIIGVAOLKKWETKNTVGNSVA-DISPSPECKNGSDEMRFREAVMRSN 119
Db 61 FAVLPLIGIVAAOLKKWETKNCVSSTNANDITOSLTKGKNDSEEMRFQEVMEHNSN 120
QY 120 MESRQYLSNEANLDAKNFQNSITDORFNDYLFQNLSSIOEHENINGDISKL 179
Db 121 MEKRIQHILDEMEANLDEHNFQNSITDORFNDYLFQNLSSVOGHNAIDEISKSL 180
QY 180 VGLNTVLDIOPSTELNGRQENAPKQZEMRKUERTYMASARIKSLDRKYLEBI 239
Db 181 ISLNTPLDQLENGLKQENTFPKQZEMRKUERTYMASARIKSLDRKYLEBI 240
QY 240 KGEMKLNNNTNDLKWDHSQTAKNTITLG 272
Db 241 KGEVKVNNNTNDLKWDHSQTAKNTITLG 273

Search completed: February 16, 2006, 17:01:04
Job time : 189 secs

Title: perfect score
Sequence:
Scoring table

US-10-618-570-2
 2059 :
 1 MAQNDDPDQEQEDTSDCTES..... DWKATRVRGINFTRLTKQE 400
 : BLOSUM62
 Gapop 10.0 , Gapext 0.5
 283416 Begr. 96216763 residues
 (without alignments) 962.168 Million cell updates/sec

1000 J. C. H. CHANG

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2	667
2	1356
2	570
2	908

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R;Kodama, T.; Freeman, M.; Rohrer, L.; Zabreesky, J.; Matsudaira, P.; Kriger, M.
Nature 343, 531-535, 1990
A;Title: Type I macrophage scavenger receptor contains alpha-helical and collagen-like
A;Reference number: S08276; MRID:90136965; PMID:2300204
A;Accession: S08276
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1453 <KOD>
A;Cross-references: UNIPROT:P21758; UNIPARC:UPI000125685; GB:X51689; GB:X54182; NID:973
A;Note: Part of this sequence was confirmed by protein sequencing
C;Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
C;Keywords: alternative splicing; coiled coil; glycoprotein; transmembrane protein
P;51-76/Domain: transmembrane #status predicted <NIN>
P;349-452/Domain: scavenger receptor cysteine-rich domain homology <SRC>
P;82,101,142,183,220,248,266/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 67.1%; Score 1381; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 4e-79; 0; Mismatches 0; Indels 0; Gaps 0;
Matcher 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matched 1 MAQWDDPPDQOEDTDSCTESYKFDARSVTALLPPHPKNGPTLQERNSYKITALITYLIV 60
1 MAQWDDPPDQOEDTDSCTESYKFDARSVTALLPPHPKNGPTLQERNSYKITALITYLIV 60
Qy 61 FVFLVPLIGIVAAQQLKKWETKNTCTGSVNADISPREGKNGSEDEMFRREAMVREMSNM 120
61 FVFLVPLIGIVAAQQLKKWETKNTCTGSVNADISPREGKNGSEDEMFRREAMVREMSNM 120
Db 121 ESRQIQLSDNEANLDAKNAKPNFSTTDQRENDFVFLQNSLSSQEHENITIGDLSKLV 180
121 ESRQIQLSDNEANLDAKNAKPNFSTTDQRENDFVFLQNSLSSQEHENITIGDLSKLV 180
Qy 181 GIANTTLDQSIERTINGRQENAKQOEERKURRIYNAEAKSLDEKQVWIEQIK 240
181 GIANTTLDQSIERTINGRQENAKQOEERKURRIYNAEAKSLDEKQVWIEQIK 240
Db 241 GEMKUQIANNTIDRLKQWHEHQSTQTLKNTILQG 272
241 GEMKUQIANNTIDRLKQWHEHQSTQTLKNTILQG 272
Qy 241 GEMKUQIANNTIDRLKQWHEHQSTQTLKNTILQG 272
Db 241 GEMKUQIANNTIDRLKQWHEHQSTQTLKNTILQG 272

RESULT 3
B38415
macrophage scavenger receptor, splice form II - human
C;Species: Homo sapiens (man)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
C;Accession: B38415
R;Matsumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori, D.E.; Kodama, T.; Proc. Natl. Acad. Sci. U.S.A. 87, 9133-9137, 1990
A;Title: Human macrophage scavenger receptors: primary structure, expression, and localization
A;Reference number: A38415; MRID:91067661; PMID:2251254
A;Accession: B38415
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <MAT>
A;Cross-references: UNIPROT:P21757; UNIPARC:UPI000022863; GB:D90188; NID:9219991; PIDN: C;Comment: For an alternative splice form, see PIR:A38415.
C;Genetics: A;Gene: GDB:MRSL
A;Cross-references: GDB:128046; OMIM:153622
A;Map position: 8p22-8p22
C;Superfamily: macrophage scavenger receptor cysteine-rich domain hc
C;Keywords: alternative splicing; coiled coil; transmembrane protein

Query Match 50.6%; Score 1042.5; DB 2; Length 358;
Best Local Similarity 72.2%; Pred. No. 4.5e-59; 34; Indels 1; Gaps 1;
Matches 197; Conservative 41; Mismatches 1;

Qy 1 MAQWDDPPDQOEDTDSCTESYKFDARSVTALLPPHPKNGPTLQERNSYKITALITYLIV 60
1 MAQWDDPPDQOEDTDSCTESYKFDARSVTALLPPHPKNGPTLQERNSYKITALITYLIV 60
1 MEQWDHFNQOEDTDSCTESYKFDARSVTALLPPHPKNGPTLQERNSYKITALITYLIV 60

Db	241 KGEVKVLANTIDRLKDWEHSOTLNITLQG	273	Db	1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV	60
RESULT 5			Qy	61 FVVLVPIGIVAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119	
A44407	macrophage scavenger receptor, splice form II - rabbit		Db	61 FAVLPIITAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119	
C;Species: <i>Oryctolagus cuniculus</i> (domestic rabbit)			Qy	120 MERSIQYLSDEANLDAKNTQNFSTTDORFDNDVLFQNSLSSIQEHENIGDISKSL 179	
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999			Db	121 MEKRIQYISDTEENLWDSEHQNFSTTDORFDADVLQSLTVPTVQGHNADEITSL 180	
C;Accession: A44407			Qy	180 VGLNTTVDLQFSIETNGRYTQENAKQOENRKLFRITVYMASBETKSLDKQVLEQI 239	
R;DOI: T. J. Higashino, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T.; Nakamura, H.; Uesugi, S.			Db	181 ISLNTTLDLHYVETLNKQFQENTLKGQBSKURKVRHNAEIMSMKREQVLEQI 240	
A;Title: Charged collagen structure mediates the recognition of negatively charged macro			Qy	240 KGEVKVLANTIDRLKDWEHSOTLNITLQG 272	
A;Reference number: A44407; MUID:93131972; PMID:8380589			Db	241 KREVKVLANTIDRLKDWEHSOTLNITLQG 273	
A;Status: preliminary; not compared with conceptual translation					
A;Molecule type: nucleic acid					
A;Residues: 1-54 <P01>					
A;Cross-references: UNIPARC:UPI0000176ED3					
A;Experimental source: lung					
A;Note: sequence extracted from NCBP backbone (NCBIP:123206)					
C;Superfamily: macrophage scavenger receptor cysteine-rich domain hc					
C;Keywords: alternative splicing					
F;350-453/Domain: scavenger receptor cysteine-rich domain homology					
Query Match Similarity 48.3%; Score 994.5; DB 2; Length 454;					
Best Local Similarity 69.2%; Pred. No. 6.2e-55; R:Matches 189; Conservative 44; Mismatches 39; Indels 1; Gaps 1;					
Qy 1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV 60					
Db 1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV 60					
Qy 61 FVVLVPIGIVAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119					
Db 61 FAVLPIITAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119					
Qy 120 MERSIQYLSDEANLDAKNTQNFSTTDORFDNDVLFQNSLSSIQEHENIGDISKSL 179					
Db 121 MEKRIQYISDTEENLWDSEHQNFSTTDORFDADVLQSLTVPTVQGHNADEITSL 180					
Qy 180 VGLNTTVDLQFSIETNGRYTQENAKQOENRKLFRITVYMASBETKSLDKQVLEQI 239					
Db 181 ISLNTTLDLHYVETLNKQFQENTLKGQBSKURKVRHNAEIMSMKREQVLEQI 240					
Db 240 KGEVKVLANTIDRLKDWEHSOTLNITLQG 272					
Db 241 KREVKVLANTIDRLKDWEHSOTLNITLQG 273					
RESULT 6					
I46833 macrophage scavenger receptor, splice form II - rabbit					
C;Species: <i>Oryctolagus cuniculus</i> (domestic rabbit)					
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004					
C;Accession: I46833					
R;BICKEL, P.B.; Freeman, M.W.					
J. Clin. Invest. 90, 1450-1457, 1992					
A;Title: Rabbit aortic smooth muscle cells express inducible macrophage scavenger receptor					
A;Reference number: I46832; MUID:93016877; PMID:1401078					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Cross-references: UNIPROT:Q05585; UNIPARC:UPI0000125687; GB:L11693; NID:9165508; PIDN F;350-453/Domain: scavenger receptor cysteine-rich domain homology					
Query Match Similarity 48.0%; Score 987.5; DB 2; Length 454;					
Best Local Similarity 68.9%; Pred. No. 1.7e-54; R:Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;					
Qy 1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV 60					
Db 1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV 60					
Qy 61 FVVLVPIGIVAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119					
Db 61 FAVLPIITAAQLKWMKNTGCTGSVNA-ISPSPKGKNSDDEMFRREAWERMNS 119					
Qy 120 MERSIQYLSDEANLDAKNTQNFSTTDORFDNDVLFQNSLSSIQEHENIGDISKSL 179					
Db 121 MEKRIQYISDTEENLWDSEHQNFSTTDORFDADVLQSLTVPTVQGHNADEITSL 180					
Qy 180 VGLNTTVDLQFSIETNGRYTQENAKQOENRKLFRITVYMASBETKSLDKQVLEQI 239					
Db 181 ISLNTTLDLHYVETLNKQFQENTLKGQBSKURKVRHNAEIMSMKREQVLEQI 240					
Db 240 KGEVKVLANTIDRLKDWEHSOTLNITLQG 272					
Db 241 KREVKVLANTIDRLKDWEHSOTLNITLQG 273					
RESULT 8					
I73338 macrophage scavenger receptor, splice form II - mouse					
C;Species: <i>Mus musculus</i> (house mouse)					
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 22-Oct-1999					
C;Accession: I73338; B38260					
R;ASHKENAS, J.; PERNAN, M.; VASILE, E.; ACTON, S.; FREEMAN, M.W.; KRIEGER, M.					
J. Lipid Res. 34, 983-1000, 1993					
A;Title: Structures and high and low affinity ligand binding properties of murine type II					
A;Cross-references: UNIPROT:Q05585; UNIPARC:UPI00002A264; GB:L11692; NID:9165510; PIDN: I73338					
C;Keywords: alternative splicing					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Residues: 1-54 <B1C>					
A;Molecule type: mRNA					
A;Cross-references: UNIPROT:Q05585; UNIPARC:UPI00002A264; GB:L11692; NID:9165510; PIDN: I73338					
Query Match Similarity 48.0%; Score 987.5; DB 2; Length 354;					
Best Local Similarity 68.9%; Pred. No. 1.2e-54; R:Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;					
Qy 1 MAQWDDPQDQDTSCEVSFKDARSTNTALLPPNPKGPPQKLKSKKALITYLLV 60					

A;Reference number: I56334; MUID:93359922; PMID:8394866
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-350 <RES>
 A;Cross-references: UNIPARC:UPI000163855; GB:L01275; NID:9293747; PMID:AAA39748.1; PID:
 R;Freeman, M.; Ashkenas, J.; Rees, D.J.G.; Kingsley, D.M.; Copeland, N.G.; Jenkins, N.A.
 proc. Natl. Acad. Sci. U.S.A. 87, 8810-8814, 1990
 A;Title: An ancient, highly conserved family of cysteine-rich protein domains revealed by
 A;Reference number: A38260; MUID:91062370; PMID:197839
 A;Accession: B38260
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 345-350 <FRE>
 A;Cross-references: UNIPARC:UPI00016CCCB; GB:MS5446; GB:M36818; NID:9192739; PMID:AAA37
 C;Superfamily: macrophage scavenger receptor; scavenger receptor cysteine-rich domain hc
 C;Keywords: alternative splicing

 Query Match 38.9%; Score 801; DB 2; Length 350;
 Best Local Similarity 59.4%; Pred. No. 5.7e-43; Matches 158; Conservative 46; Mismatches 2; Gaps 2;
 Qy 8 PDQEQPDTSCTESVKEDRSVTAALPDPHPKNGQPTIQERMKSYKTAUTLIVFVLVPI 67
 Db 9 PHERERPADCCSSESVKEDRSVTAALPDPHPKNGQPTIQERMKSYKTAUTLIVFVLVPI 68
 Qy 68 IGVIAVQQLKNETKNTGVSUN-ADSPSPGKGKGSDEDMFRKAVMERMSNMESRIOY 126
 Db 69 VGIIVTAQQLNEMKNCVCSRNTSDTSQGPMEKNTSVNEMRF-TTMARHMKDMEKRIQS 127
 Qy 127 LSDNEANLLDAKKNFQNSITIDQRFIDVFLRLNSLSSIQHENHNLGDIKSLVQVLLTV 186
 Db 128 ISNKADLIDPGRFQFQNSMADTQRLNDLQLNLSVQBGHNSLDAISKLQSLANMIL 187
 Qy 187 LDQFQSIETLNGVQDQNAFKQOBEMKLEREELYNASAETKSLDEKQVYEQEIKEMKUL 246
 Db 188 LDVQLHETELVVRVRASTAKQEDDSKLEERYVKSREVSQVKERQAHVEQEVKOBVRV 247
 Qy 247 NNITNDLRLKOWEHSTQTKNITLQG 272
 Db 248 NNITNDLRLKOWEHSTQTKNITLQG 273

 RESULT 9
 B44407
 macrophage scavenger receptor, splice form I - mouse
 N;Alternate names: macrophage scavenger receptor type I
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: B44407; A38260; 156334
 R;DOI: T. Higashima, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T.; Nakamura, H.; Uesugi, S.
 J. Biol. Chem. 268, 2126-2133, 1993
 A;Title: Charged collagen structure mediates the recognition of negatively charged macro
 A;Reference number: A44407; PMID:93131972; PMID:8380589
 A;Accession: B44407
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-458 <DOI>
 A;Cross-references: UNIPROT:R32024; UNIPARC:UPI0000293B4
 A;Experimental source: macrophage cell line R38BD
 A;Note: sequence extracted from NCBI backbone (NCBIP:23207)
 R;Freeman, M.; Ashkenas, J.; Rees, D.J.G.; Kingsley, D.M.; Copeland, N.G.; Jenkins, N.A.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8810-8814, 1990
 A;Title: An ancient, highly conserved family of cysteine-rich protein domains revealed by
 A;Reference number: A38260; MUID:91062370; PMID:197839
 A;Accession: A38260
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 349-458 <FRE>
 A;Cross-references: UNIPARC:UPI00016CCCA; GB:MS5445; GB:MS6817; NID:9192737; PMID:AAA37
 R;Ashkenas, J.; Freeman, M.; Vaille, E.; Acton, S.; Freeman, M.W.; Krieger, M.
 J. Lipid Res. 34, 983-1000, 1993
 A;Title: Structures and high and low affinity ligand binding properties of murine type I
 A;Reference number: A38260; MUID:91062370; PMID:197839

Db 83 QPTFGPTVHWNFSESTSVFVGQCFDRSGKEVLUKTKWLQLAVLDDWKAATRVGYNF 142
 Qy 393 TRLRTQKE 400
 Db 143 TRQRTVEE 150

RESULT 13

S42201 avidin-related protein 1 precursor - chicken
 N;Alternate names: avrl
 C;Species: Gallus gallus (chicken)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S42201
 R;Kainonen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkonen, M.O.; Toimela, T.A.; Helenius, E.; J. Biochem. 220, 615-621, 1994
 A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
 A;Reference number: S42201; MUID:91170814; PMID:812512
 A;Accession: S42201
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-150 <KEI>
 A;Cross-references: UNIPROT:O13153; UNIPARC:UPI0000126670; EMBL:Z21611
 C;Genetics:
 A;Introns: 27/3; 95/1; 136/2
 C;Superfamily: avidin
 C;Subfamily: avidin
 C;Keywords: glycoprotein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-150/Product: avidin-related protein 1 #status predicted <MAT>
 F;25-150/Disulfide bonds: #status predicted <WAT>
 Query Match 22.0%; Score 452; DB 2; Length 150;
 Best Local Similarity 68.8%; Pred. No. 1.3e-21;
 Matches 88; Conservative 10; Mismatches 28; Indels 2; Gaps 1;
 Qy 273 ARKCSITGKWNLDLSNMITGAVNRGEFTGTYITAVTATSNESNEKESPLHGTTQNTINKRT 332
 Db 25 ARKCSITGKWNLDLSNMITGAVNRGEFTGTYITAVTATSNESNEKESPLHGTTQNTINKRT 332
 Qy 333 QPTFGPTVHWNFSESTSVFVGQCFDRSGKEVLUKTKWLQLAVLDDWKAATRVGYNF 392
 Db 83 QPTFGPTVHWNFSESTSVFVGQCFDRSGKEVLUKTKWLQLAVLDDWKAATRVGYNF 392
 Qy 393 TRLRTQKE 400
 Db 143 TRQRTVEE 150

RESULT 14

S42202 avidin-related protein 2 precursor - chicken
 N;Alternate names: avr2 protein
 C;Species: Gallus gallus (chicken)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S42202; S39799
 R;Kainonen, R.A.; Wallen, M.J.; Kristo, P.A.; Laukkonen, M.O.; Toimela, T.A.; Helenius, E.; J. Biochem. 220, 615-621, 1994
 A;Title: Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5.
 A;Reference number: S42201; MUID:91170814; PMID:812512
 A;Accession: S42202
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-150 <KEI>
 A;Cross-references: UNIPROT:P1079; UNIPARC:UPI000016C068; GB:X17530; NID:910225; PMID:9640136
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-14
 A;Accession: B40136
 A;Cross-references: UNIPARC:UPI000017BB23
 A;Status: preliminary
 A;Cross-references: UNIPARC:UPI000017BB23
 R;Hurbsh, D.A.; Andrews, M.E.; Raff, R.A.
 Science 237, 1487-1490, 1987
 A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
 A;Reference number: A29316; MUID:87319677; PMID:3498216
 A;Accession: A29316
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 181-251, 329-370, 'R', 372-408, 'RA', 411-441 <DE2>
 A;Accession: C40136
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 'K', 747-821, 898-978 <DE3>
 A;Cross-references: UNIPARC:UPI000017BB23
 R;Hurbsh, D.A.; Andrews, M.E.; Raff, R.A.
 Science 237, 1487-1490, 1987
 A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
 A;Reference number: A29316; MUID:87319677; PMID:3498216
 A;Accession: A29316
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: UNIPARC:UPI000016C06A; GB:MI17421; PIDN:AAA30050.1; PID:R;Hunt, L.T.; Barker, W.C.
 FASEB J. 3, 1760-1764, 1989
 A;Title: A avidin-like domain in an epidermal growth factor homolog from a sea urchin.
 A;Reference number: A43131; MUID:89198806; PMID:2784773
 A;Contents: annotation
 C;Comments: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
 F;1-13/Domain: signal sequence #status predicted <SIG>
 F;20-1064/Product: fibropellin I #status predicted <FIB>
 F;21-54/Domain: EGF homology <EG1>
 F;55-175/Domain: C1r/C1s repeat homology <C1r>
 F;180-211/Domain: EGF homology <EG2>

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:

February 16, 2006, 16:58:02 ; Search time 231 Seconds

{without alignments} 1221.694 Million cell updates/sec

Title: US-10-618-570-2

Perfect score: 2059

Sequence: 1 MAQWDDFPDQQEDTDSCTES.....DWKATRGINIFTRLRQKE 400

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched:

2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05-00:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1381	67.1	453	1 MSRR_BOVIN
2	1042.5	50.6	388	2 O6E0505_HUMAN
3	1042.5	50.6	451	1 MSRR_HUMAN
4	987.5	48.0	454	1 MSRR_RABBIT
5	830	40.3	354	2 Q8C6D7_MOUSE
6	801	38.9	458	1 MSRR_MOUSE
7	675	32.9	152	1 AVID_CHICK
8	664	32.2	152	1 Q98SH4_CHICK
9	491	23.8	150	1 AVR4_CHICK
10	483.5	23.5	122	2 Q8AY75_MELGIA
11	461	22.4	150	1 AVR3_CHICK
12	461	22.4	150	1 AVR7_CHICK
13	452	22.0	150	1 AVR1_CHICK
14	451	21.9	150	1 AVR6_CHICK
15	436	21.2	150	1 AVR2_CHICK
16	233	11.3	95	2 P70111_MESAU
17	219	10.6	499	2 Q5RFW0_BRARE
18	204	9.9	400	2 Q8n4Z7_HUMAN
19	204	9.9	495	2 Q6ZM47_HUMAN
20	199.5	9.7	374	2 Q9CUC2_MOUSE
21	199.5	9.5	491	2 Q91W66_MOUSE
22	194.5	9.4	387	2 Q8BZZ2_MOUSE
23	194.5	9.4	491	2 Q8K299_MOUSE
24	173.5	8.4	410	2 Q4RF52_TETR
25	164.5	8.0	357	2 Q7Z4A1_HUMAN
26	163.5	7.9	280	2 Q9D4G8_MOUSE
27	144	7.0	283	2 Q8R330_MOUSE
28	144	7.0	1190	2 Q519A0_ENTH1
29	141.5	6.9	778	2 Q96WJ2_KLUY
30	141	6.8	980	2 Q73ML2_TREDE
31	6.8	1064	1 FBP1_STRPV	P10079 strongly

ALIGMENTS

32	139.5	6.8	183	1 SAVI_STRLV	053533 streptomyce
33	138.5	6.7	183	1 SAVI_STRLV	053532 streptomyce
34	138.5	6.7	183	1 SAVI_STRLV	P22629 streptomyce
35	138.5	6.7	947	2 Q6LF09_PLAF7	06105 plasmidium
36	136	6.6	529	2 Q25058_HELER	025058 helicocardi
37	135.5	6.6	9439	2 Q8CP76_STAEP	08cp76 staphylococ
38	135.5	6.6	10203	2 QSHPA2_STAEQ	05hpaz staphylococ
39	133.5	6.5	715	2 Q51542_HORBU	051542 borrelia bu
40	132.5	6.4	466	2 Q8R3F2_MOUSE	08r3f2 mus musculus
41	132.5	6.4	543	2 Q8BMK2_MOUSE	Q8bmka mus musculus
42	132.5	6.4	570	2 Q97FD7_CLOAB	097fd7 clostridium
43	132.5	6.4	1163	1 SBCC_GIQAQ	Q4s759 tetrandon n
44	132	6.4	657	2 Q4S759_TETNG	Q6khx4 mycoplasma
45	132	6.4	1461	2 Q6khx4_MYCQMO	Q6khx4 mycoplasma

RESULT 1

MSRE_BOVIN

STANDARD; PRT; 453 AA.

ID MSRE_BOVIN

AC P21758;

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Macrophage scavenger receptor types I and II (Macrophage acetylated LDL receptor I and II).

GN Name=MSRL;

OS Bos taurus (Bovine);

OC Bubalida; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherida; Laurasiatheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos.

RN NCBI_TaxID=9913;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=90136965; PubMed=2300204; DOI=10.1038/343531a0;

RX Kodama T., Freeman M., Rohrer L., Matsudaira P., Krieger M.,

RX "Type I macrophage scavenger receptor contains alpha-helical and collagen-like coiled coils.";

RX Nature 343:531-535 (1990).

RX [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).

RC TISSUE=Lung;

RX MEDLINE=90136973; PubMed=2300208; DOI=10.1038/343570a0;

RX Rohrer L., Freeman M., Kodama T., Penman M., Krieger M.,

RX "Coiled-coil fibrous domain mediate ligand binding by macrophage scavenger receptor type II.";

RX Nature 343:570-572 (1990).

CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic deposition of cholesterol in arterial walls during atherosclerosis. Two types of receptor subunits exist. These receptors mediate the endocytosis of a diverse group of macromolecules, including modified low density lipoproteins (LDL).

CC -1- SUBUNIT: Homotrimer.

CC -1- SUBCELLULAR LOCATION: Type II membrane protein.

CC -1- ALTERNATIVE PRODUCTS: Event:Alternative splicing; Named isoforms=2;

CC Name=I;

CC ISoID=P21758-1; Sequence=Displayed;

CC Name=II;

CC ISoID=P21758-2; Sequence=VSP_006227; VSP_006228;

CC -1- SIMILARITY: Contains 1 collagen-like domain.

CC -1- SIMILARITY: Contains 1 SICR domain.

CC

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DR	EMBL; X51689; CNA35987.1; - ; mRNA.	AC	060505;	
DR	EMBL; X54183; CNA38108.1; - ; mRNA.	DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)	
DR	EMBL; S08276; S08276.	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DR	PIR; S08278; S08278.	DR	Macrophage scavenger receptor type III.	
DR	InterPro; IPR00160; Collagen.	DR	Hom sapiens (Human).	
DR	InterPro; IPR00160; Collagen.	DR	Homo sapiens (Human).	
DR	InterPro; IPR003543; Macscav receptor.	DR	Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	InterPro; IPR001190; Ssrc_receptor.	DR	Makarysta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
DR	PANTHER; PHMR1931;SP5; Macscav_receptor; 1.	DR	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
DR	Pfam; PF01391; Collagen; 1.	DR	Homino.	
DR	Pfam; PF03523; Macscav_rec; 1.	DR	Homino.	
DR	Pfam; PF00330; Ssrc; 1.	DR	NCBi_TaxID=9606;	
DR	PRINTS; PRO1408; MACCAVRCPR.	DR	[1]	
DR	PRINTS; PRO00258; SPERACTRCPR.	RP	NUCLEOTIDE SEQUENCE.	
DR	PRINTS; PRO00007; C1g helix; 1.	RX	MEDLINE-98208366; PubMed=9548586;	
DR	SMART; SM00202; SR; 1.	RA	Gough P.J.; Greaves D.R.; Gordon S.;	
DR	PROSITE; PS00420; SRR_1; 1.	RT	"A naturally occurring isoform of the human macrophage scavenger receptor (SR-A) gene generated by alternative splicing blocks modified LDL uptake."; J. Lipid Res. 39:531-543 (1998).	
DR	PROSITE; PS00287; SRR_2; 1.	RT	DR	Ensembl; ENSG00000038945; Homo sapiens.
FT	TOPO_DOM	FT	DR	GO; GO:0005737; C:cytoplasm; IEA.
FT	TRANSMEM	FT	DR	GO; GO:0016030; C:membrane; IEA.
FT	DOMAIN	FT	DR	GO; GO:0004872; F:receptor activity; IEA.
FT	REGION	FT	DR	GO; GO:0005044; F:scavenger receptor activity; IEA.
FT	COILED	FT	DR	GO; GO:0006817; P:phosphate transport; IEA.
FT	CARBONID	FT	DR	GO; GO:0006828; P:receptor mediated endocytosis; IEA.
FT	CARBONID	FT	DR	InterPro; IPR00161; C1g helix.
FT	CARBONID	FT	DR	InterPro; IPR008160; Collagen.
FT	CARBONID	FT	DR	InterPro; IPR00343; Macscav receptor.
FT	CARBONID	FT	DR	InterPro; IPR001190; Ssrc receptor.
FT	CARBONID	FT	DR	Pfam; PF01391; Collagen; 1.
FT	CARBONID	FT	DR	Pfam; PF03523; Macscav_rec; 1.
FT	CARBONID	FT	DR	PRINTS; PRO1408; MACCAVRCPR.
FT	CARBONID	FT	DR	PRINTS; PRO00258; SPERACTRCPR.
FT	DISUFDID	FT	DR	PRODOM; PD000007; C1g helix; 1.
FT	DISUFDID	FT	DR	SMART; SM00202; SR; 1.
FT	DISUFDID	FT	DR	PROSITE; PS00287; SRR_2; 1.
FT	VARSPLIC	FT	DR	Collagen; Receptor.
FT	VARSPLIC	FT	DR	SEQUENCE 388 AA; D6A20BCE57BFBC46 CRC64;
FT	SEQUENCE	FT	DR	SEQUENCE 453 AA; 50057 MW; 77A0FEE4B00A21 CR64;
FT	SEQUENCE	FT	DR	Missing (In isoform II). /FTId=SP 006228.
Query Match	Best Local Similarity 67.1%; Score 1381; DB 1; Length 453; Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match	Best Local Similarity 50.6%; Score 1042.5; DB 2; Length 388; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;	
Qy	1 MAQWDDPFQDQEDTSCSKEVSKEDARSVTALPPHKNGPTQKERMKSXTKALITYLV 60	Qy	1 MAQWDDPFQDQEDTSCSKEVSKEDARSVTALPPHKNGPTQKERMKSXTKALITYLV 60	
Db	1 MAQWDDPFQDQEDTSCSKEVSKEDARSVTALPPHKNGPTQKERMKSXTKALITYLV 60	Db	1 MAQWDDPFQDQEDTSCSKEVSKEDARSVTALPPHKNGPTQKERMKSXTKALITYLV 60	
Qy	61 FVVLVPLIGIVAAQKLNKETKNTGVSNTDPSPKGNGSDEMRPRAEMRMSNM 120	Qy	61 FVVLVPLIGIVAAQKLNKETKNTGVSNTDPSPKGNGSDEMRPRAEMRMSNM 119	
Db	61 FVVLVPLIGIVAAQKLNKETKNTGVSNTDPSPKGNGSDEMRPRAEMRMSNM 120	Db	61 FVVLVPLIGIVAAQKLNKETKNTGVSNTDPSPKGNGSDEMRPRAEMRMSNM 120	
Qy	121 ESRIQWISDNNEANLLDAKNFQNSITTDQRFNDVLFQNLNSLASSIQLQHENIGDLSILV 180	Qy	120 MESRIQWISDNNEANLLDAKNFQNSITTDQRFNDVLFQNLNSLASSIQLQHENIGDLSI 179	
Db	121 ESRIQWISDNNEANLLDAKNFQNSITTDQRFNDVLFQNLNSLASSIQLQHENIGDLSILV 180	Db	121 MERKIOHILDMANLMDTEHQNFSMTDQRFNDVLFQNLNSLASSIQLQHENIGDLSI 180	
Qy	181 GIANTVLDQFSETLNGVQENAFQKOBEMRKLERIYNAESAEIKSLDEKOVYLBOK 240	Qy	180 GIANTVLDQFSETLNGVQENAFQKOBEMRKLERIYNAESAEIKSLDEKOVYLBOK 239	
Db	181 GIANTVLDQFSETLNGVQENAFQKOBEMRKLERIYNAESAEIKSLDEKOVYLBOK 240	Db	181 ISLNTTLDQFSETLNGVQENAFQKOBEMRKLERIYNAESAEIKSLDEKOVYLBOK 240	
Qy	241 GEMKLUANNITNDLRLKOMEWEHSQTLKNITLQG 272	Qy	240 GEMKLUANNITNDLRLKOMEWEHSQTLKNITLQG 272	
Db	241 GEMKLUANNITNDLRLKOMEWEHSQTLKNITLQG 272	Db	241 GEVKVLUANNITNDLRLKOMEWEHSQTLKNITLQG 273	

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CC CC CC

DR EMBL; L11633; AAA31402.1; -; mRNA.

DR EMBL; L11632; AAA31403.1; -; mRNA.

DR EMBL; D13381; BAA02649.1; -; mRNA.

DR PIR; I46862; I46862.

DR PIR; I46863; I46863.

DR InterPro; IPR008161; Clg_helix.

DR InterPro; IPR00160; Collagen.

DR InterPro; IPR00543; Macrocav receptor.

DR InterPro; IPR001190; Srcr_receptor.

DR PANTHER; PTHR19331; P5; Macscav_receptor; 1.

DR Pfam; PF01391; Collagen; 1.

DR Pfam; PF03523; Macscavre; 1.

DR Pfam; PF00330; SRCR; 1.

DR PRINTS; PRO1408; MACSCAVCPTR.

DR PRINTS; PRO0258; SPERACTCPTR.

DR PRODOM; PDD00007; CIG_helix; 1.

DR SMART; SM00202; SR; 1.

DR PROSITE; PS50240; SSCR_1; 1.

KW Alternative splicing; Coiled coil; Collagen; Endocytosis;

KW Glycoprotein; LDL_Receptor; Signal-anchor; Transmembrane.

FT TOPO_DOM 1 50 Signal-anchor for type II membrane

FT TRANSMEM 51 73

FT TOPO_DOM 74 454

FT DOMAIN 273 344

FT DOMAIN 353 453

FT REGION 74 109

FT COILED 199 256

FT CARBOHYD 82 82

FT CARBOHYD 102 102

FT CARBOHYD 143 143

FT CARBOHYD 184 184

FT CARBOHYD 221 221

FT CARBOHYD 249 249

FT CARBOHYD 267 267

FT DISULFID 378 442

FT DISULFID 391 452

FT DISULFID 422 432

FT VARSPIC 348 354

FT VARSPIC 355 454

FT CONFLICT 105 106

FT SEQUENCE 454 AA; 49745 MW; 521A79632EA76429 CRC64;

Query Match 48.0%; Score 987.5; DB 1; Length 454;

Best Local Similarity 68.9%; Pred. No. 1.4e-51;

Matches 188; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

QY 1 MAQWDDDPDQDDEDTCTESVFKDARSVTALLPPHEKNGTQLQERMVSKYKLTALITLILV 60

QY 1 MAQWDDDPDQDDEDTCTESVFKDARSVTALLPPHEKNGTQLQERMVSKYKLTALITLILV 60

QY 61 FVFLVLPVIGTVAQQLKWEKNTKNTGVSNAID-TSPSPKGKONGSDEPMEFREAMRMSN 119

QY 61 FAVLPLTIAAQLKWEKNTGVSNAID-TSPSPKGKONGSDEPMEFREAMRMSN 119

QY 120 MESRICQLSNEANLILDAKQFQNSFITSITDORFNDVLFQNLNSLSSIQEHENIGDLSKL 179

QY 121 MEKRGQYISDTEENLVNDSEHOFNSFVTDORFADYLQLOSLTLPVQHGNADVBITSL 180

QY 180 VGLNTTVLUDLOFSIETNGRVQENAFKQQEMRKUEERIVNASABIKSLSDEKQVILQEI 239

QY 240 KGEMKUJLNTINDLRKDWHESQTJNITLQG 272

QY 241 KREVKVJLNTINDLRKDWHESQTJNITLQG 273

QY 181 ISLNTTJLNLHJYETLNVKFQENTLKGQEBISKURKERVINASABIMSMKQEQLVLEQI 240

DE Macrophage scavenger receptor types I and II (Macrophage acetylated
DE LDL receptor I and II) (Scavenger receptor type A) (SR-A).
GN Name=Mar1; Synonyms=Scrv;
OS Mus musculus (Mouse);
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorpha;
OC Muroidea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10590;
OX [11] RX NUCLEOTIDE SEQUENCE (ISOFORMS I AND II).
RX MEDLINE=3359822; PubMed=8394868;
RX J. Lipid Res. 34:983-1000(1993).
RN "Structures and high and low affinity ligand binding properties of
RT murine type I and type II macrophage scavenger receptors.";
RL Ashkenas J., Penman M., Vasile E., Acton S., Freeman M.W., Krieger M.;
RN [2] RX NUCLEOTIDE SEQUENCE (ISOFORM II).
RN MEDLINE=93131972; PubMed=8380589;
RN Doi T., Wada Y., Kodama T., Higashi K.I., Kurihara Y., Miyazaki T.,
RA Nakamura H., Uesugi S., Imanishi T., Kawabe Y., Itakura H., Yasaki Y.,
RA Matsumoto A.;
RT "Charged collagen structure mediates the recognition of negatively
RT charged macromolecules by macrophage scavenger receptors.";
RL J. Biol. Chem. 268:2126-2133(1993).
RN [3] RX NUCLEOTIDE SEQUENCE (ISOFORM I).
RN STRAIN=CB7BL/6;
RN Rateri D.L., Whitman S.C., Block A.E., Daugherty A.;
RT "Identification of a functional domain in class A scavenger receptors
RT that mediates metabolism of AcLDL";
RN Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [4] RX NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RN STRAIN=NOD; TISSUE="Thymus";
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiido T., Osato N., Saito R., Suzuki H., Yamamoto T., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanazawa A., Matsuda H., Batalov S., Belsel K.W.,
RA Blaue J.A., Bradt D., Brusic V., Chothia C., Corhann L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grinberg S., Gustincic S., Hirakawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lehardt B., Lyons P.A.,
RA Maglott D.R., Maltos L., Marchionni L., McHenry L., Miki H.,
RA Nageshima T., Numata K., Okido T., Pavan W.J., Peretz G., Pebole G.,
RA Petrovsky N., Pillai R., Ponius J.D., Qil D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Seton M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang J., Yang L.,
RA Yuzan Z., Zavilok M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume K.,
RA Shiraki T., Waki K., Kawai J., Alizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa T.,
RA Miyazaki A., Sakai A., Sasada D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length DNAs.;"
RL Nature 420:563-573(2002).
RN [5] RX NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM II).
RX MEDLINE=2338857; PubMed=12471932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krausneker R.D., Collins F.S., Wagner L., Sheehan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heise F.,
RA Blatchko L., Matsushina K., Farmer A.A., Rubin G.M., Hong L.,
RT Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RN

RA Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Logueillo P.N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McBwan P.J., McKernan J.H., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heitton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A./
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6] RX NUCLEOTIDE SEQUENCE OF 349-458.
RX MEDLINE=91062370; PubMed=1978939;
RA Freeman M., Ashkenas J., Dore D.J., Kingsley D.M., Copeland N.G.,
RA Jenkins N.A., Krieger M.;
RT "An ancient, highly conserved family of cysteine-rich protein domains
RT revealed by cloning type I and type II murine macrophage scavenger
RT receptors";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8810-8814(1990).
RN [7] RX NUCLEOTIDE SEQUENCE OF 1-4.
RX MEDLINE=95395388; PubMed=7666008;
RA Afting R.P., Freeman M.W.;
RT "Structure of the murine macrophage scavenger receptor gene and
RT evaluation of sequences that regulate expression in the macrophage
RT cell line, P388D.;"
RL J. Lipid Res. 36:1305-1314(1995).
CC -1- FUNCTION: Membrane glycoproteins implicated in the pathologic
CC deposition of cholesterol in arterial walls during atherosclerosis.
CC Two types of receptor subunits exist. These receptors mediate the
CC endocytosis of a diverse group of macromolecules, including
CC modified low density lipoproteins (LDL).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
CC Name=I; IsoId=p30204-1; Sequence=Displayed;
CC Name=II;
CC IsoId=p30204-2; Sequence=VSP_005231; VSP_006232;
CC -1- SIMILARITY: Contains 1 collagen-like domain.
CC -1- SIMILARITY: Contains 1 SRCR domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L04274; AA39747.1; ALT_INIT; mRNA.
DR EMBL; L04275; AA39748.1; ALT_INIT; mRNA.
DR EMBL; D13382; BA02650.1; mRNA.
DR EMBL; AF203781; AA1F14001.1; mRNA.
DR EMBL; M94445; AA37464.1; mRNA.
DR EMBL; M9446; AA37465.1; mRNA.
DR EMBL; U13873; AAC3774.1; Genomic_DNA.
DR EMBL; AK089178; BAC40779.1; mRNA.
DR EMBL; BC003814; AAB03814.1; mRNA.
DR PIR; B44407; B44407.
DR Ensembl; ENSMUSG0000025044; Mus musculus.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR008161; CIG_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR0353; Macscav_receptor.
DR InterPro; IPR002197; Spectrin.
DR InterPro; IPR001190; Scrv_receptor.
DR Panther; PTIHL9331;SF5; Macscav_receptor; 1.
DR Pfam; PF01391; Collagen; 1.

Qy	333	OPTFGFTVNWKESESTTVFTGOCFIDRNGKEVLTWMILLRSVNDIGDDWATRGINIF	392	Qy	333	OPTFGFTVNWKESESTTVFTGOCFIDRNGKEVLTWMILLRSVNDIGDDWATRGINIF	392
Db	85	OPTFGFTVNWKFSESTTVFTGOCFIDRNGKEVLTWMILLRSVNDIGDDWATRGINIF	144	Db	83	OPTFGFTVWNKFSESTTVFTGOCFIDRNGKEVLTWMILLRSVNDIGDDWATRGINIF	142
Qy	393	TRLTQKE 400		Qy	393	TRLTQKE 400	
Db	145	TRLTQKE 152		Db	143	TRLCTVEE 150	
	RESULT 9				RESULT 10		
	AVR4 CHICK	STANDARD;	PRT;	150 AA.		Q8AY76_MELGA	
ID	P56734;				ID	Q8AY76_MELGA PRELIMINARY;	PRT;
AC					AC	Q8AY76;	
DT	30-MAY-2000 (Rel. 39, Created)				DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)				DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	13-SEP-2005 (Rel. 48, Last annotation update)				DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE	Avidin-related protein 4/5 precursor.				DE	Avidin (Fragment)	
GN	Name=AVR4;				OS	Meleagris gallopavo (Common turkey).	
GN	Name=AVR5;				RA	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OS	Gallus gallus (Chicken).				RA	Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RN	NCBI_TaxID=9103;	
OC	Archosauia; Aves; Neognathae; Galliformes; Phasianidae;				RP	NUCLEOTIDE SEQUENCE.	
OX	Gallus.				RP	MEDLINE=2275582; PubMed=12672662; DOI=10.1093/biolreprod.102.015172;	
RN	[1]				RA	Long B.L., Sonstegard T.S., Long J.A., Van Tassel C.P., Zuelke K.A., in	
RP	NUCLEOTIDE SEQUENCE.				RA	"Serial analysis of gene expression in turkey sperm storage tubules in	
RC	STRAIN=White Leghorn; TISSUE=Oviduct;				RT	the presence and absence of resident sperm.";	
RX	MEDLINE=4170814; PubMed=8125122;				RL	Biol. Reprod. 69:469-474 (2003).	
RA	Keinonen R.A., Wallen M.J., Kistlo P.A., Laukkanen M.O.,				DR	EMBL: AF58546; AAC38297.1; -; mRNA.	
RA	Toimela T.A., Helminen M.A., Kulomaa M.S.;				DR	HSSP; P02201; INQN.	
RT	"Molecular cloning and nucleotide sequence of chicken avidin-related				DR	SMR; Q8AY76; 28-122.	
RT	genes 1-5,"				DR	InterPro; IPR005469; Avidin.	
RL	Eur. J. Biochem. 220:615-621 (1994).				DR	InterPro; IPR005468; Avidin/st.	
CC	-1- MISCELLANEOUS: The sequences of the coding regions of genes AVR4				DR	PRAM; PF01382; Avidin; 1.	
CC	and AVR5 are identical.				DR	PRINTS; PR00709; AVIDIN.	
CC	-1- SIMILARITY: Belongs to the avidin/streptavidin family.				PT	NON_TER 122 122	
CC					SQ	SEQUENCE 122 AA; 13368 MW; 3D22EE74480E97E0 CRC64;	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				Query Match	23.5%; Score 483.5; DB 2; Length 122;	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				Best Local Similarity	82.9%; Pred. No. 8.1e-22;	
CC	the European Bioinformatics Institute. There are no restrictions on its				Matches	92; Conservative 8; Mismatches 8; Indels 3; Gaps 1;	
CC	use as long as its content is in no way modified and this statement is not						
CC	removed.						
DR	EMBL; Z22883; -, NOT_ANNOTATED_CDS; Genomic_DNA.				Qy	264 LKNITL--OGARKCSSLGKNDLGSNMIGAVNSRGEFTGTVITAVATNEIKEESP	320
DR	PIR; S42204; S42204; Y				Db	12 LLSLALNAPGHSAKKCLLTKWINDLGSNMIGAVNSRGEFTGTVITAVATNSIKEESP	71
DR	PDB; 1Y52; X-ray; XY=25-150.				Qy	321 LHGTONTTNGKTOPFGFTVNWKFESTTVTGFDRIDRNGKEVLTWMIL 371	
DR	PDB; 1Y55; X-ray; XY=25-150.				Db	72 LYGTQNNNNKKQOPTFGFTVNWKFESTTVTGFDRIDRNGKEVLTWMIL 122	
DR	Ensembl; ENSGALG000000241; Gallus gallus.						
DR	InterPro; IPR005469; Avidin.						
DR	InterPro; IPR005468; Avidin/st.						
DR	Pfam; PF01382; Avidin; 1.						
DR	PRINTS; PR00709; AVIDIN.						
DR	PROSITE; PS00577; AVIDIN.						
KW	3D-structure; Biotin; Glycoprotein; Multigene family; signal.						
FT	SIGNAL 1 24 Potential.						
FT	CHAIN 25 150 Avidin-related protein 4/5.						
FT	BINDING 57 57 Biotin (By similarity).						
FT	67 N-linked (GlcNAc. . .) (Potential).						
FT	93 N-linked (GlcNAc. . .) (Potential).						
FT	141 141 N-linked (GlcNAc. . .) (Potential).						
SEQUENCE	150 AA; 16644 MW; 9A66C6310E8E13A CRC64;						
	Query Match 23.8%; Score 491; DB 1; Length 150;						
	Best Local Similarity 76.6%; Pred. No. 3.7e-22; Gaps 1;						
	Matches 98; Conservative 7; Mismatches 21; Indels 2;						
Qy	273 ARKCSITGKWTNDLGSNMIGAVNSRGEFTGTVITAVATNEIKEESPHTGONTINKRT						
Db	25 ARKCSLTGKWTNDLGSNMIGAVNSRGEFTGTVLTAVADNEGNITLSPLGQH--KRAS						
	82						

RT genes 1-5.";
 RL Eur. J. Biochem. 220:615-621(1994).
 CC -; SIMILARITY: Belongs to the avidin/streptavidin family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 removed.
 CC
 CC EMBL; Z22612; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; Z22612; -; NOT_ANNOTATED_CDS; mRNA.
 DR IRI; S42203; S42203.
 DR HSSP; P0201; INQN.
 DR SMR; P56733; 26-147.
 DR Ensembl; ENSGALG0000002441; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PRINTS; PR00719; AVIDIN.
 DR PROSITE; PR00577; AVIDIN; 1.
 KW Biotin; Glycoprotein; Multigene family; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 150 Avidin-related protein 3.
 FT BINDING 57 Biotin (By similarity).
 FT CARBOHYD 93 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 141 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 150 AA; 16657 MW; 840C03926AB21C CRC64;
 Best Local Similarity 71.1%; Pred. No. 2.4e-20;
 Matches 91; Conservative 10; Mismatches 25; Indels 2; Gaps 1;
 QY 273 ARKCSLTGKWNFDLSNMIGAVNRRGEFCTYITAVTANSNEKESPLHGTONINKRT 332
 Db 25 ARKCSLTGKWNFDLSNMIGAVNRRGEFCTYITAVTANSNEKESPLHGTONINKRT 332
 QY 333 OPTRGPTVWKPKSESTTVFGQCPIDRNGKEVLTWMILLASSVNDIGDPMKATRGINIP 392
 Db 83 OPTRGPTVWKPKSESTTVFGQCPIDRSGKEVLTWMILLASSVNDIGDPMKATRGINIP 142
 QY 393 TRLRTQKE 400
 Db 143 TRQRTVEE 150
 RESULT 12
 AVR7_CHICK STANDARD; PRT; 150 AA.
 ID AVR7_CHICK
 AC P56736; Q9W64;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DT Avidin-related protein 7 precursor.
 GN Name=AVR7;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Rhode Island.
 RX MEDLINE=21070478; PubMed=11167523;
 RA Ahroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R.,
 RA Kulomaa M.S.;
 RA "Characterization and chromosomal localization of the chicken avidin
 gene family";
 RA Anim. Genet. 31:367-375(2000);
 RA -; SIMILARITY: Belongs to the avidin/streptavidin family.
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 CC
 DR EMBL; AU237659; CAB39894.1; -; Genomic_DNA.
 DR HSSP; P02701; INQN.
 DR SMR; P56733; 26-147.
 DR Ensembl; ENSGALG0000002441; Gallus gallus.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR Pfam; PF01382; Avidin; 1.
 DR PROSITE; PR00577; AVIDIN; 1.
 DR Biotin; Glycoprotein; Multigene family; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 150 Avidin-related protein 7.
 FT BINDING 57 Biotin (By similarity).
 FT CARBOHYD 41 41 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 54 54 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 93 93 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 141 141 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 150 AA; 16543 MW; 30F33611F65923D CRC64;
 Best Local Similarity 70.3%; Pred. No. 2.4e-20;
 Matches 90; Conservative 10; Mismatches 26; Indels 2; Gaps 1;
 QY 333 OPTRGPTVWKPKSESTTVFGQCPIDRNGKEVLTWMILLASSVNDIGDPMKATRGINIP 392
 Db 83 OPTRGPTVWKPKSESTTVFGQCPIDRSGKEVLTWMILLASSVNDIGDPMKATRGINIP 142
 QY 273 ARKCSLTGKWNFDLSNMIGAVNRRGEFCTYITAVTANSNEKESPLHGTONINKRT 332
 Db 25 ARKCSLTGKWNFDLSNMIGAVNRRGEFCTYITAVTANSNEKESPLHGTONINKRT 332
 QY 333 OPTRGPTVWKPKSESTTVFGQCPIDRNGKEVLTWMILLASSVNDIGDPMKATRGINIP 392
 Db 83 OPTRGPTVWKPKSESTTVFGQCPIDRSGKEVLTWMILLASSVNDIGDPMKATRGINIP 142
 QY 393 TRLRTQKE 400
 Db 143 TRQRTVEE 150
 RESULT 13
 AVR1_CHICK STANDARD; PRT; 150 AA.
 ID AVR1_CHICK
 AC O13153;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Avidin-related protein 1 precursor.
 Name=AVR1;
 GN Gallus gallus (Chicken).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oviduct;
 RX MEDLINE=88260103; PubMed=2838690; DOI=10.1016/0022-4731(88)90071-4;
 RA Keinonen R.A., Laukkanen M.-L., Kulomaa M.S.;
 RA "Molecular cloning of three structurally related genes for chicken
 avidin.,"
 RA J. Steroid Biochem. 30:17-21(1988).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=White Leghorn; TISSUE=Oviduct;
 RX MEDLINE=94170814; PubMed=8125122;
 RA Keinonen R.A., Wahlen M.J., Kristo P.A., Laukkanen M.O.,
 RA Toivola T.A., Heleenius M.A., Kulomaa M.S.;
 RA "Molecular cloning and nucleotide sequence of chicken avidin-related
 genes 1-";
 RA Eur. J. Biochem. 220:615-621(1994);
 CC -; SIMILARITY: Belongs to the avidin/streptavidin family.

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; 221611; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; 297063; CAB09198.1; -; mRNA.
 DR PIR; S42201; S42201.
 DR HSSP; P02101; INQN.
 DR Ensemble; ENSGA00000000241; Gallus gallus.

DR InterPro; IPR005469; Avidin.

DR InterPro; IPR005468; Avidin/str.

DR Pfam; PF01382; Avidin_1.

DR PRINTS; PS00577; AVIDIN_1.

DR PROSITE; PS00577; AVIDIN_1.

DR PROSTB; PS00577; AVIDIN_1.

DR BIOTIN; Glycoprotein; Multigene family; Signal.

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein.

DR BINDING_57; 57 Avidin-related protein.

DR CARBOHYD_54; 54 Biotin (By similarity).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16468 MW; 775483805995BF6 CRC64;

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein 1.

DR BINDING_57; 57 Biotin (By similarity).

DR CARBOHYD_54; 54 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16528 MW; C0F3357D6291B150 CRC64;

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein 1.

DR BINDING_57; 57 Biotin (By similarity).

DR CARBOHYD_54; 54 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16468 MW; 775483805995BF6 CRC64;

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein.

DR BINDING_57; 57 Avidin-related protein.

DR CARBOHYD_54; 54 Biotin (By similarity).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16468 MW; 775483805995BF6 CRC64;

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein.

DR BINDING_57; 57 Avidin-related protein.

DR CARBOHYD_54; 54 Biotin (By similarity).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16468 MW; 775483805995BF6 CRC64;

DR SIGNAL_1; 24 Potential.

DR CHAIN_25; 150 Avidin-related protein.

DR BINDING_57; 57 Avidin-related protein.

DR CARBOHYD_54; 54 Biotin (By similarity).

DR CARBOHYD_67; 67 N-linked (GlcNAc. . .) (Potential).

DR CARBOHYD_93; 93 N-linked (GlcNAc. . .) (Potential).

DR SEQUENCE_150 AA; 16468 MW; 775483805995BF6 CRC64;

Query Match 22.0%; Score 452; DB 1; length 150;
 Best Local Similarity 68.8%; Pred. No. 8. 4e-20;
 Matches 88; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 273 ARKCSLTGKWTNDLGSNTTGA VNSRGEFTGTYTAVADNGNITRSPLOGI OH--KRAC 392

Db 25 ARKCSLTGKWTNDLGSNTTGA VNSRGEFTGTYTAVADNGNITRSPLOGI OH--KRAC 82

QY 333 OPTFGFTVWNKFSESTIVFGCPI DRNGKEVLTWMLASSVNDGDDWKA TRGIVNIF 392

Db 83 OPTFGFTVWNKFSESTIVFGCPI DRNGKEVLTWMLASSVNDGDDWKA TRGIVNIF 142

QY 393 TRLRTCKE 400

Db 143 TRQRTVBE 150

RESULT 14

ID AVR6_CHICK STANDARD; PRT; 150 AA.

AC P56735; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Avidin-related protein 6 precursor.

GN Name=AVR6;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

NCBI_TAXID=9031;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=White Leghorn; TISSUE=oviduct;

RC MEDLINE=94170814; PubMed=8125122;

RA Keinonen R.A., Wallen M.J., Kristo P.A., Laukkanen M.O., Toimela T.A., Heilman M.A., Kulomaa M.S.,

RT "Molecular cloning and nucleotide sequence of chicken avidin-related genes 1-5"; Genes 1-5;, Eur. J. Biochem. 220:615-621(1994).

RA Ahlroth M.K., Kola E.H., Ewald D., Masabanda J., Sazanov A., Fries R., Kulomaa M.S.;

RT "Characterization and chromosomal localization of the chicken avidin gene family"; Anim. Genet. 31:367-375(2000).

RL "Similiarity: Belongs to the avidin/streptavidin family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

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DR EMBL; Z31554; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; 221535; -; NOT_ANNOTATED_CDS; mRNA.
DR EMBL; AU331648; CAC34570; 1; -; Genomic_DNA.
DR PIR; S42202; S42202.
DR HSPB; P02701; INQN.
DR Ensembl; ENSGALG00000002441; Gallus gallus.
DR InterPro; IPR05469; Avidin.
DR InterPro; IPR05468; Avidin/str.
DR Pfam; PF01382; Avidin; 1.
DR PRINTS; PRO0709; AVIDIN.
DR PROSITE; PS00577; AVIDIN; 1.
DR Biotin; Glycoprotein; Multigene family; Signal.
FT SIGNAL; 1 24 Potential.
FT CHAIN 25 150 Avidin-related protein 2.
FT BINDING 57 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 67 67 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc. . .) (Potential).
FT SEQUENCE 150 AA; 16435 MW; 7631E8B1A93A66D CRC64;
Query Match 21 2%; Score 436; DB 1; Length 150;
Best Local Similarity 57.2%; Pred. No. 7; 8e-19;
Matches 86; Conservative 11; Mismatches 29; Indels 2; Gaps 1;
QY 273 ARKSSLTGKWMNDLGSNSMTIGAVNSRGERFTGTYTAVATSNKESPLHGTONTINKRT 332
Db 25 ARKSSLTGKWMNDLGSNSMTIGAVNSRGERFTGTYTAVATSNKESPLHGTONTINKRT 332
QY 333 QPTRGFTVNPKPSSESTVFTGQCRPDRNGKEVULKTMWLRSSVNDIDGDDWKAATRVGNTF 392
Db 83 QPTGFPTVHWNFSESTSIVFVGQCFVDRSGKEVLLKWLQLAVLDDIISDDWIATRVGNDF 142
Qy 393 TRLRQKE 400
Db 143 TRQHTEEE 150

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 16, 2006, 17:05:18 ; Search time 47 Seconds

703.623 Million cell updates/sec

Title: US-10-618-570-2
Perfect score: 2059
Sequence: 1 MAQWDDFPDQQEDTDSCTES.....DNKATRGINIFTRLR7QKE 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 sqs, 8267579 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata1/1/aa/5_COMB_pep: *
2: /cgn2_6/prodata1/1/aa/6_COMB_pep: *
3: /cgn2_6/prodata1/1/aa/H_COMB_pep: *
4: /cgn2_6/prodata1/1/aa/PCTUS_COMB_pep: *
5: /cgn2_6/prodata1/1/aa/RE_COMB_pep: *
6: /cgn2_6/prodata1/1/aa/backfile1_pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 1381 67.1 349 6 5510466-2 Patent No. 5510466

2 1381 67.1 453 6 5510466-4 Patent No. 5510466

3 1047.5 50.9 451 1 US-08-154-365-2 Sequence 2, Appli

4 1042.5 50.6 358 1 US-08-453-177-4 Sequence 4, Appli

5 1042.5 50.6 358 1 US-08-948-222-4 Sequence 4, Appli

6 1042.5 50.6 358 1 US-08-973-145-4 Sequence 4, Appli

7 1042.5 50.6 358 1 PCT-US56-08081-4 Sequence 4, Appli

8 1042.5 50.6 362 4 US-09-949-016-9288 Sequence 4, Appli

9 1042.5 50.6 451 1 US-08-453-117-2 Sequence 2, Appli

10 1042.5 50.6 451 1 US-08-948-222-4 Sequence 2, Appli

11 1042.5 50.6 451 1 US-08-973-145-4 Sequence 2, Appli

12 1042.5 50.6 451 2 US-09-276-010-10 Sequence 10, Appli

13 1042.5 50.6 451 2 US-09-448-056-10 Sequence 4, Appli

14 1042.5 50.6 451 2 US-09-702-772-10 Sequence 10, Appli

15 1042.5 50.6 451 4 PCT-US56-08081-2 Sequence 2, Appli

16 1042.5 50.6 451 4 US-09-366-862-4 Sequence 2, Appli

17 1042.5 50.6 452 2 US-09-831-399-4 Sequence 2, Appli

18 1042.5 50.6 452 2 US-09-368-772-4 Sequence 2, Appli

19 1042.5 50.6 459 2 US-08-628-550-1 Sequence 17, Appli

20 1042.5 50.6 459 2 US-08-948-097-17 Sequence 1, Appli

21 1042.5 50.6 459 2 US-08-941-100-1 Sequence 5, Appli

22 1042.5 50.6 459 2 US-08-941-100-5 Sequence 2, Appli

23 1042.5 50.6 459 2 US-09-381-330-2 Sequence 2, Appli

24 1042.5 50.6 459 2 US-08-831-399-2 Sequence 2, Appli

25 1042.5 50.6 459 2 US-09-366-862-2 Sequence 2, Appli

26 1042.5 50.6 459 2 US-09-368-772-2 Sequence 2, Appli

27 1042.5 50.6 459 2 PCT-US53-05240-14 Sequence 14, Appli

RESULT 1
5510466-2
; Patent No. 5510466
; APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO
; TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
; THERETO
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,400
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 997,113
; FILING DATE: 24-DEC-1992
; APPLICATION NUMBER: 391,486
; FILING DATE: 09-AUG-1989
; APPLICATION NUMBER: 292,002
; FILING DATE: 15-NOV-1988
; SEQ ID NO:2:
; LENGTH: 349

Patent No. 5160499
Sequence 7, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 9, Appli
Sequence 3159, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1252, Appli
Sequence 1252, Appli

Query Match 67.1%; Score 1381; DB 6; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-112; Indels 0; Gaps 0;
Matches 272; Conservative 0; Mismatches 0;
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QY 1 MAQWDDFPDQQEDTDSCTESTKFDARSTVALLPPRKNGTQERMKSYKTTALITYLV 60
; 1 MAQWDDFPDQQEDTDSCTESTKFDARSTVALLPPRKNGTQERMKSYKTTALITYLV 60
Db 1 MAQWDDFPDQQEDTDSCTESTKFDARSTVALLPPRKNGTQERMKSYKTTALITYLV 60
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; 61 FVVLVPIIGIVAAQQLKWEKNTGVSNAIDISPPEKGKNGSEDEMREAAVERMNN 120
Db 61 FVVLVPIIGIVAAQQLKWEKNTGVSNAIDISPPEKGKNGSEDEMREAAVERMNN 120
; 121 ESRIOQISDNENALIADKNFNSITTDORFENDVFLQNLNSLSSIOBHENITGDISLV 180
; 121 ESRIOQISDNENALIADKNFNSITTDORFENDVFLQNLNSLSSIOBHENITGDISLV 180
Db 121 ESRIOQISDNENALIADKNFNSITTDORFENDVFLQNLNSLSSIOBHENITGDISLV 180
; 181 GLANTTVDLQFSIETNGRYVQENAKQEQEMKLUERITMNAEIKSLBKQVYLEQIK 240
; 181 GLANTTVDLQFSIETNGRYVQENAKQEQEMKLUERITMNAEIKSLBKQVYLEQIK 240
Db 181 GLANTTVDLQFSIETNGRYVQENAKQEQEMKLUERITMNAEIKSLBKQVYLEQIK 240
; 241 GEMKLUINNTDLRKDWEHQTSQTLKNTLQG 272
; 241 GEMKLUINNTDLRKDWEHQTSQTLKNTLQG 272
Db 241 GEMKLUINNTDLRKDWEHQTSQTLKNTLQG 272
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RESULT 2
5510466-4
; Patent No. 5510466
; APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO

; TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
 ; THESE TO
 ; NUMBER OF SEQUENCES: 12
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/307,400
 ; FILING DATE: 16-SEP-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 997,113
 ; FILING DATE: 24-DEC-1992
 ; APPLICATION NUMBER: 301,486
 ; FILING DATE: 09-AUG-1989
 ; APPLICATION NUMBER: 272,002
 ; FILING DATE: 15-NOV-1988
 ; SEQ ID NO:4:
 ; SEQ ID NO:4:
 ; LENGTH: 453
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 ; Query Match 67.1%; Score 1381; DB 6; Length 453;
 ; Best Local Similarity 100.0%; Pred. No. 6.3e-112; Mismatches 0; Indels 0; Gaps 0;
 ; Matches 272; Conservative 0; Mismatches 0;
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 Db 1 MAQWDDFPDQOEDTSDCTESVKFDRSVAATLLPFPKNGPTLQERMKSYKTAITLYLIV 60
 ;
 QY 61 FVVLVPIIGTVAAQIWKWETKNTGVSNAIDSPSPKGNSDEMRFREAVMRSMN 120
 Db 61 FVVLVPIIGTVAAQIWKWETKNTGVSNAIDSPSPKGNSDEMRFREAVMRSMN 120
 ;
 QY 121 ESRIOYLSDNENALIQLAKNFTNSITDORNDVFOLNLSIISQEHENTIGDISKLV 180
 Db 121 ESRIOYLSDNENALIQLAKNFTNSITDORNDVFOLNLSIISQEHENTIGDISKLV 180
 ;
 QY 181 GLANTTLLDQSFETLNGRVQENAPKQEMRKLERIYMASAETKSLDKQVILEQETK 240
 Db 181 GLANTTLLDQSFETLNGRVQENAPKQEMRKLERIYMASAETKSLDKQVILEQETK 240
 ;
 QY 241 GEMKUJNNITNDLRKWEHSQTKNITLQG 272
 Db 241 GEMKUJNNITNDLRKWEHSQTKNITLQG 272
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 RESULT 3
 US-08-154-365-2
 ; Sequence 2, Application US/08154365
 ; Patent No. 5624904
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Dunn, Dana W.
 ; APPLICANT: Reznick, David
 ; APPLICANT: Kreiger, Monty
 ; APPLICANT: Joiner, Keith A.
 ; TITLE OF INVENTION: Method for Treating Gram-Positive
 ; TITLE OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 1100 Peachtree Street, Suite 2800
 ; CITY: Atlanta
 ; STATE: Ga
 ; COUNTRY: USA
 ; ZIP: 30309-4530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/154,365
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: MITC392
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404)-815-6508
 ; TELEFAX: (404)-815-6555
 ; INFORMATION FOR SEQ ID NO: 2:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: homo sapien
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Ashkenas, et al.
 ; JOURNAL: J. Lipid Res.
 ; VOLUME: 34
 ; PAGES: 983-1000
 ; DATE: 1993
 ;
 ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 451
 ; US-08-154-365-2
 ;
 ; Query Match 50.9%; Score 1047.5; DB 1; Length 451;
 ; Best Local Similarity 72.5%; Pred. No. 7.4e-83; Mismatches 34; Indels 1; Gaps 1;
 ; Matches 198; Conservative 40; Mismatches 34; Indels 1; Gaps 1;
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 QY 1 MAQWDDFPDQOEDTSDCTESVKFDRSVAATLLPFPKNGPTLQERMKSYKTAITLYLIV 60
 Db 1 MAQWDDFPDQOEDTSDCTESVKFDRSVAATLLPFPKNGPTLQERMKSYKTAITLYLIV 60
 ;
 QY 61 FVVLVPIIGTVAAQIWKWETKNTGVSNAIDSPSPKGNSDEMRFREAVMRSMN 119
 Db 61 FVVLVPIIGTVAAQIWKWETKNTGVSNAIDSPSPKGNSDEMRFREAVMRSMN 119
 ;
 QY 120 MESRQYLSDNENALIQLAKNFTNSITDORNDVFOLNLSIISQEHENTIGDISKLV 179
 Db 121 MEKRIOYLSDNENALIQLAKNFTNSITDORNDVFOLNLSIISQEHENTIGDISKLV 180
 ;
 QY 180 VGLANTTLLDQSFETLNGRVQENAPKQEMRKLERIYMASAETKSLDKQVILEQET 239
 Db 181 ISLANTTLLDQSFETLNGRVQENAPKQEMRKLERIYMASAETKSLDKQVILEQET 240
 ;
 QY 240 GEMKUJNNITNDLRKWEHSQTKNITLQG 272
 Db 241 GKEVKKUJNNITNDLRKWEHSQTKNITLQG 273
 ;
 ;
 ; RESULT 4
 ; US-08-453-117-4
 ; Sequence 4, Application US/08453117
 ; Patent No. 5683903
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Lysko, Paul G.
 ; APPLICANT: Elshourbagy, Nabil A.
 ; APPLICANT: Brawner, Mary E.
 ; TITLE OF INVENTION: Attachment Enhanced 293 Cells
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham - Corporate Patents
 ; ADDRESSEE: U.S.
 ; STREET: Mailcode - UW2220, 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-5090
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/453,117
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: SIC-P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5019
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-453-117-4

Query Match 50.6%; Score 1042.5; DB 1; Length 358;
 Best Local Similarity 72.2%; Pred. No. 1.4e-82; DB
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

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 Db 1 MEQWDHFHNQDQBDTDSCESEVKFDARSMTALLPPNPKNSPLQEKLUFSKRALIALYLV 60

Qy 61 FVVLVLTIGIVAAQLIKWETKNTCVSVNA-DISPEREGKNGSEDEMRFREAVMRNS 119
 Db 61 FAVLPLIGIVAAQLIKWETKNTCVSVNSVSTNANDITQSLTGKNDSEEMRQEYVEMHSN 120

Qy 120 MERSIQYLDSDBNLDAKNQNFSITDQRFNDVFLQNLSSIOBHENIGDISKL 179
 Db 121 MEKRIQHLDMEANLMDTEHQFSNTDQRFNDLQLSITFSSYQGHGAIDEISKSL 180

Qy 180 VGLNTTVDIOPSIETNGRYOENAQQEMRKLERIYVYASAEEKSLSDEKQVYQEI 239
 Db 181 ISLNTTLDLQNIENANGKIQENTPKQBLISKUBERVYVNSAEMAKBEOVHLEQI 240

Qy 240 KGEKMULNNTIDLRJKDWEHSQTQKNTLQG 272
 Db 241 KGEVKULNNTIDLRJKDWEHSQTQKNTLQG 273

RESULT 5
 US-08-948-222-4
 Sequence 4, Application US/08948222
 ; Patent No. 5863798
 GENERAL INFORMATION:
 ; APPLICANT: Lysko, Paul G.
 ; APPLICANT: Elshourbagy, Nabil A.
 ; APPLICANT: Browner, Mary E.
 ; TITLE OF INVENTION: Attachment Enhanced 293 Cells
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Smithkline Beecham - Corporate Patents
 ; ADDRESSER: U.S.
 ; STREET: Mailcode - UW220, 709 SwedeIand Road
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-5090
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; CURRENT APPLICATION NUMBER: US/08/948,222
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/453,117

PILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: SIC-P50338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5019
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-948-222-4

Query Match 50.6%; Score 1042.5; DB 1; Length 358;
 Best Local Similarity 72.2%; Pred. No. 1.4e-82; DB
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

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 Db 1 MEQWDHFHNQDQBDTDSCESEVKFDARSMTALLPPNPKNSPLQEKLUFSKRALIALYLV 60

Qy 61 FVVLVLTIGIVAAQLIKWETKNTCVSVNA-DISPEREGKNGSEDEMRFREAVMRNS 119
 Db 61 FAVLPLIGIVAAQLIKWETKNTCVSVNSVSTNANDITQSLTGKNDSEEMRQEYVEMHSN 120

Qy 120 MERSIQYLDSDBNLDAKNQNFSITDQRFNDVFLQNLSSIOBHENIGDISKL 179
 Db 121 MEKRIQHLDMEANLMDTEHQFSNTDQRFNDLQLSITFSSYQGHGAIDEISKSL 180

Qy 180 VGLNTTVDIOPSIETNGRYOENAQQEMRKLERIYVYASAEEKSLSDEKQVYQEI 239
 Db 181 ISLNTTLDLQNIENANGKIQENTPKQBLISKUBERVYVNSAEMAKBEOVHLEQI 240

Qy 240 KGEKMULNNTIDLRJKDWEHSQTQKNTLQG 272
 Db 241 KGEVKULNNTIDLRJKDWEHSQTQKNTLQG 273

RESULT 6
 US-08-973-145-4
 Sequence 4, Application US/08973145
 ; Patent No. 5319636
 GENERAL INFORMATION:
 ; APPLICANT: Lysko, Paul G.
 ; APPLICANT: Elshourbagy, Nabil A.
 ; APPLICANT: Browner, Mary E.
 ; TITLE OF INVENTION: Attachment Enhanced 293 Cells
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Smithkline Beecham - Corporate Patents U.S.
 ; STREET: Mailcode - UW220, 709 SwedeIand Road
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-5090
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/973,145
 ; FILING DATE: 26-Nov-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Elizabeth J. Hecht
 ; REGISTRATION NUMBER: P-41, 824
 ; REFERENCE/DOCKET NUMBER: P50338
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 270-5009

TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 356 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-4

Query Match 50.6%; Score 1042.5; DB 1; Length 358;
 Best Local Similarity 72.2%; Pred. No. 1.4e-82;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQMDPDPQQEDTSCTESVKFARSVTALLPPHPKNGTQERMKSYTALITYLIV 60
 Db 1 MEQWHFHNGQBDTDSCEVKFARSVTALLPPHPKNSLQEKIKSPKAALITYLIV 60

Qy 61 FVVLVPIGIVAAQQLKWEKNTCTVGSVNA-DISPSPKGNSDEMRFREAVMRMSN 119
 Db 61 FAVLPLIGIVAAQQLKWEKNTCTVGSVNA-DISPSPKGNSDEMRFREAVMRMSN 119

Qy 120 MESRIOQLSNEANLDAKQFQNSFTDORFENDVLFQFOLNSLSSIOEHENIGDISKL 179
 Db 121 MEKRIQHILDMEANLMDTEHFQNSFTDORFNDLQILQSTLFLSSVQHNAIDBISKL 180

Qy 180 VGLNTVLDIQLQFSTLRLNRVQENAFPKQCEMRKLEERYNASEBRIKSIDEKQYLEQI 239
 Db 181 ISLNTTLDIQLQNTENLNGKIQENTPKQCEMRKLEERYNASEBRIKSIDEKQYLEQI 239

Qy 240 KGEMKLNNNTNDLRLKWEHSQTLRNTLQG 272
 Db 241 KGEMKLNNNTNDLRLKWEHSQTLRNTLQG 272

Qy 241 KGEVKVLNNNTNDLRLKWEHSQTLRNTLQG 273

RESULT 7
 PCT-US96-08081-4

Sequence 4. Application PC/TUS9608081
 GENERAL INFORMATION:
 APPLICANT: SmithKline Beecham Corporation
 TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4

Correspondence Address:
 ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UW2220, 709 Swedeland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5090

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/08081
 FILING DATE: 1996-08-01
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 REGISTRATION NUMBER: 31,171
 REFERENCE/DOCKET NUMBER: P50338
 ATTORNEY/AGENT INFORMATION:
 NAME: Jervis, Herbert H.
 TELEPHONE: (610) 270-5019
 TELEFAX: (610) 270-0900
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-08081-4

Query Match 50.6%; Score 1042.5; DB 4; Length 358;

RESULT 9
 US-00453-117-2
 ; Sequence 2, Application US/08453117
 ; Patent No. 583903
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyko, Paul G.
 ; APPLICANT: Elsbourbagy, Nabil A.
 ; TITLE OF INVENTION: Attachment Enhanced 293 Cells
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham - Corporate Patents
 ; ADDRESSEEE: U.S.
 ; STREET: Mailcode - UW2220, 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19406-5090
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/453,117
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jervis, Herbert H.
 ; REGISTRATION NUMBER: 31,171
 ; REFERENCE/DOCKET NUMBER: SBC-P50338
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 270-5019
 ; TELEFAX: (610) 270-5090
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-00453-117-2
 ;
 ; Query Match 50.6%; Score 1042.5; DB 1; Length 451;
 ; Best Local Similarity 72.2%; Pred. No. 2e-82; 1;
 ; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
 ;
 ; Qy 1 MAQWDDDPDQDQDTSCTESVKDARSVTALLPPNPKNSPSLQEKUKSKKALIALYLIV 60
 ; Db 1 MEQWDHFRNQQDQDTSCTESVKDARSVTALLPPNPKNSPSLQEKUKSKKALIALYLIV 60
 ;
 ; Qy 61 FVFLVPLIGIVAAQLKMETKNTCTGVNA-DISPFEGKNGSEDEMFRREAVMRMSN 119
 ; Db 61 FAVLPLIGIVAAQLKMETKNGSVSNTNANDITOSITGKNDSEBEMRFOEVMEHMSN 120
 ;
 ; Db 61 FAVLPLIGIVAAQLKMETKNGSVSNTNANDITOSITGKNDSEBEMRFOEVMEHMSN 120
 ;
 ; Qy 61 FVFLVPLIGIVAAQLKMETKNTCTGVNA-DISPFEGKNGSEDEMFRREAVMRMSN 119
 ; Db 61 FAVLPLIGIVAAQLKMETKNGSVSNTNANDITOSITGKNDSEBEMRFOEVMEHMSN 120
 ;
 ; Qy 120 MESRIQLSDNEANLDAKFNQFSITDQRNDVIFQNLSSQHEHENIGDISKL 179
 ; Db 121 MEKRIQHILDEANLMTEHFRQFSMFTDQRNDVIFQNLSSQHGNGNADEISKL 180
 ;
 ; Qy 180 VGLNTVLDLOPSIETLNGRVOENAFTQQEENRKLEERIYMASAETKSLDERQVYIEQI 239
 ; Db 181 ISLNTTLDLOANIENINGKQENTFKQOEISKLEERVVNSAEMAKBQVHLEQI 240
 ;
 ; Qy 240 XGEMKLNNTNDLKDWEISOTKNTLQG 272
 ; Db 181 ISLNTTLDLOANIENINGKQENTFKQOEISKLEERVVNSAEMAKBQVHLEQI 240
 ; Db 241 KGEVKVLANNTNDLKDWEHSQTLRNLTQG 273
 ;
 ; RESULT 10
 ; US-00-948-222-2
 ; Sequence 2, Application US/08948222
 ; Patent No. 5833798
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyko, Paul G.
 ; APPLICANT: Elsbourbagy, Nabil A.
 ;
 ; RESULT 11
 ; US-08-973-145-2
 ; Sequence 2, Application US/08973145
 ; Patent No. 5919636
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyko, Paul G.
 ; APPLICANT: Elsbourbagy, Nabil A.
 ;
 ; RESULT 12
 ; US-08-973-145-2
 ; Sequence 2, Application US/08973145
 ; Patent No. 5919636
 ; GENERAL INFORMATION:
 ; APPLICANT: Brawner, Mary E.
 ; APPLICANT: Brawner, Mary E.

TITLE OF INVENTION: Attachment Enhanced 293 Cells
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Smithkline Beecham - Corporate Patents U.S.
 STREET: Mailcode - UW2220, 709 Swedesland Road
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19406-5090
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,145
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth J. Hecht
 REGISTRATION NUMBER: P-41, 824
 REFERENCE/DOCKET NUMBER: PS-0338
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5009
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-973-145-2

Query Match 50.6%; Score 1042.5; DB 1; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
 Matches 197; Conservatory 41; Mismatches 34; Indels 1; Gaps 1;
 Qy 1 MAQWDDPQDQEDTSCTESVKFDRSVTALLPPRKNGPTLQERNKSYKTAITYLIV 60
 Db 1 MEQWDHFHNQEDTSCSSEVKFDRSMTALLPPRKNSLSQEKSKFKAIALYLV 60
 Qy 120 MESRQLQISDNEANLDAKOFQNSITTDQRENDFULQNLSSLSIQEHENIGISSL 179
 Db 121 MEKROHILDMEANLMDTEHONFNTTDFRNDFDILQIQLQSTLFFSVQHGNAIDEISKSL 180
 Qy 180 VGLNTTVDIQLQFSETIENGVOENAFQKQOBEMRKUBERYNAESAKSLDEKQVYLEQI 239
 Db 181 ISLNTTLDIQLQIENLNGKQENTPKQOBESIKUBERVINVSAIMAKEEQVHLEQI 240
 Qy 240 KGEMKLANNITNDLRLKWDHSQTLKNTLQG 272
 Db 241 KGEVKVUNNITNDLRLKWDHSQTLKNTLQG 273

RESULT 13
 US-03-448-076-10
 Sequence 10, Application US/09448076
 Patent No. 630092
 GENERAL INFORMATION:
 APPLICANT: Khodaboust, Mehran et al.
 TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
 FILE REFERENCE: MNT-073CP
 CURRENT FILING DATE: 1999-11-23
 EARLIER APPLICATION NUMBER: 60/117,580
 EARLIER FILING DATE: 1999-01-27
 EARLIER APPLICATION NUMBER: 09/276,400
 EARLIER FILING DATE: 1999-03-25
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 10
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-03-448-076-10

Query Match 50.6%; Score 1042.5; DB 2; Length 451;
 Best Local Similarity 72.2%; Pred. No. 2e-82; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
 Matches 197; Conservatory 41; Mismatches 34; Indels 1; Gaps 1;
 Qy 1 MAQWDDPQDQEDTSCTESVKFDRSVTALLPPRKNGPTLQERNKSYKTAITYLIV 60
 Db 1 MEQWDHFHNQEDTSCSSEVKFDRSMTALLPPRKNSLSQEKSKFKAIALYLV 60
 Qy 120 MESRQLQISDNEANLDAKOFQNSITTDQRENDFULQNLSSLSIQEHENIGISSL 179
 Db 121 MEKROHILDMEANLMDTEHONFNTTDFRNDFDILQIQLQSTLFFSVQHGNAIDEISKSL 180
 Qy 180 VGLNTTVDIQLQFSETIENGVOENAFQKQOBEMRKUBERYNAESAKSLDEKQVYLEQI 239
 Db 181 ISLNTTLDIQLQIENLNGKQENTPKQOBESIKUBERVINVSAIMAKEEQVHLEQI 240
 Qy 240 KGEMKLANNITNDLRLKWDHSQTLKNTLQG 272

Db 241 KGEVKVLANNTNDLRKDWEHQSTQTRNITL1QG 273

RESULT 14

US-09-702-572-10

PATENT NO. 6591602

GENERAL INFORMATION:

APPLICANT: Khoddadoust, Mehran

TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: USES THEREFOR

FILE REFERENCE: MNT-073

CURRENT APPLICATION NUMBER: US/09/702,572

CURRENT FILING DATE: 2000-10-31

PRIOR APPLICATION NUMBER: 09/276,400

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 451

TYPE: PRT

ORGANISM: Homo sapiens

US-09-702-572-10

Query Match Best Local Similarity 50.6%; Score 1042.5; DB 2; Length 451; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

QY 1 MAQWDDPPDQBDTSCTESVKFDRASVTAALLPPHRKNGPQLQERNMSKSYKATALITYLIV 60

Db 1 MEQWDHFHNQOBDTDSCESVKFDRASVTAALLPPHRKNGPQLQERNMSKSYKATALITYLIV 60

QY 61 FVVLVLIIGIVAAQLKWEKNTGIVSVA-DISPEPGKNGSEDEMFRFRAVERMSN 119

Db 61 FAVLPLIGIVAAQLKWEKNTGIVSVA-DISPEPGKNGSEDEMFRFRAVERMSN 119

QY 120 MESRIOYLSDEANLIDAKONFNSITDQFENDVFLQMSLSSQIHEHENIGISKL 179

Db 121 MEKRICHILDMEANLMDTFRONFSMTDORFNDLILQSLTFLSSVQGHNADEBISKL 180

QY 180 VGLNTVLDIQLPSIETNGRVOENAQQEMRKLERITYNASEKSLBKQVLEQI 239

Db 181 ISINTTLDIQLQNIENNGKIQENTKQEBIKLERSVYVNAEIMAKBEOVHLEQI 240

QY 240 KGEVKVLANNTNDLRKDWEHQSTQTRNITL1QG 272

Db 241 KGEVKVLANNTNDLRKDWEHQSTQTRNITL1QG 273

RESULT 15

PCT-US96-08081-2

SEQUENCE 2, Application PC/TUS9608081

GENERAL INFORMATION:

APPLICANT: SmithKline Beecham Corporation

TITLE OF INVENTION: Attachment Enhanced 293 Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: SmithKline Beecham - Corporate Patents U.S.

STREET: Mailcode - UW4220, 709 SwedeLand Road

STATE: King of Prussia

CITY: Pennsylvania

ZIP: U.S.A.

ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-POS/MS-DOS

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/08081

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

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• Qy 301 PFTGTVITAVTATSNIKESPLHLGHTONTINGRKTQPTPGFTVNWKUSBTSVFTGQCPIDRN 360
 ; Db 301 FTGTVITAVTATSNIKESPLHLGHTONTINGRKTQPTPGFTVNWKUSBTSVFTGQCPIDRN 360
 ; Qy 361 GKEVVKTMWILRSYNDIGDDKATRUGINIFTRURTOKE 400
 ; Db 361 GKEVVKTMWILRSYNDIGDDKATRUGINIFTRURTOKE 400

RESULT 2
 US-10-326-186-6
 ; Sequence 6, Application US/10326186
 ; Publication No. US20030119149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reddy, Pramitha
 ; TITLE OF INVENTION: Trimeric Recombinant Polypeptides
 ; FILE REFERENCE: 3398-A
 ; CURRENT APPLICATION NUMBER: US/10/326,186
 ; CURRENT FILING DATE: 2002-12-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq in version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-326-186-6

Query Match 50.6%; Score 1042.5; DB 4; Length 358;
 Best Local Similarity 72.2%; Pred. No. 3.1e-77; Mismatches 34; Indels 1; Gaps 1;
 Matches 197; Conservative 197; Conservative 197; Conservative 197; Conservative 197; Conservative 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQMDPPDQDIDSCTESVKPDKARSVTALLPPHKNGPTLQERMKSYKTLITYLIV 60
 ; Db 1 MEQMDHFMQEDTSCSSEVKFDARSVTALLPPKPKNSPLQEKLSKALALYLV 60

Qy 61 FVVLVPIGTVAAQLKWMETKNCVGSVNA-DTSPSPKGKNGSEDEMFRREAMERMSN 119
 ; Db 61 FAVLPIGTVAAQLKWMETKNCVGSVNA-DTSPSPKGKNGSEDEMFRREAMERMSN 119

Qy 120 MERSIQYLSNEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 179
 ; Db 120 MERSIQYLSNEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 179

Qy 121 MEKRIQHILDEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 180
 ; Db 121 MEKRIQHILDEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 180

RESULT 4
 US-10-741-600-1397
 ; Sequence 1397, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1397
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-741-600-1397

Query Match 50.6%; Score 1042.5; DB 5; Length 358;
 Best Local Similarity 72.2%; Pred. No. 3.1e-77; Mismatches 34; Indels 1; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQMDPPDQDIDSCTESVKPDKARSVTALLPPHKNGPTLQERMKSYKTLITYLIV 60
 ; Db 1 MEQMDHFMQEDTSCSSEVKFDARSVTALLPPKPKNSPLQEKLSKALALYLV 60

Qy 61 FVVLVPIGTVAAQLKWMETKNCVGSVNA-DTSPSPKGKNGSEDEMFRREAMERMSN 119
 ; Db 61 FAVLPIGTVAAQLKWMETKNCVGSVNA-DTSPSPKGKNGSEDEMFRREAMERMSN 119

Qy 120 MERSIQYLSNEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 179
 ; Db 120 MERSIQYLSNEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 179

Qy 121 MEKRIQHILDEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 180
 ; Db 121 MEKRIQHILDEANLDAKQFONFISITDORFNDLFLQFQNLSSLSI0EHENIGDISKL 180

RESULT 5
 US-10-741-600-1398
 ; Sequence 1398, Application US/10741600
 ; Publication No. US2005002169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.

FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1394
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Homo sapiens
 ; US-10-741-600-1394

Query Match 50.6%; Score 1042.5; DB 5; Length 358;
 Best Local Similarity 72.2%; Pred. No. 3.1e-77; Mismatches 34; Indels 1; Gaps 1;

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SEQ ID NO 1398
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1398

Query Match 50.6%; Score 1042.5; DB 5; Length 358;
 Best Local Similarity 72.2%; Pred. No. 3.1e-77; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPPDQOEDTDSCTESVFKDARAVTALLPPHPKNGPQLQERMSKSYKALITYLIV 60
 Db 1 MEQWDDPPDQOEDTDSCTESVFKDARAVTALLPPHPKNGPQLQERMSKSYKALITYLIV 60

Qy 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119
 Db 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119

Qy 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119
 Db 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119

Qy 120 MERSICQLSDNBANLDAKNPONFSTTIDQRENDFVPLQNSLSSQBHENIGTIDISKSL 179
 Db 120 MERSICQLSDNBANLDAKNPONFSTTIDQRENDFVPLQNSLSSQBHENIGTIDISKSL 179

Qy 121 MEKRICHILDMEANTLMDTERFQNPFSMTDQRENDFLQLSTLFSVQGHNADEISKSL 180
 Db 121 MEKRICHILDMEANTLMDTERFQNPFSMTDQRENDFLQLSTLFSVQGHNADEISKSL 180

Qy 180 VGLNTTFLDQSFIEETLGRVQENAKRQEEENRKLERIRYMAEAKSLDERKQVIRQEI 239
 Db 181 ISLNTTFLDQSFIEETLGRVQENAKRQEEENRKLERIRYMAEAKSLDERKQVIRQEI 239

Qy 240 KGMKMLNNTTDLRKDWEHSOTLKNITLQG 272
 Db 240 KGMKMLNNTTDLRKDWEHSOTLKNITLQG 272

Qy 241 KGEVKYLNNTTDLRKDWEHSOTLKNITLQG 273
 Db 241 KGEVKYLNNTTDLRKDWEHSOTLKNITLQG 273

RESULT 6
 US-10-741-600-1396
 Sequence 1395, Application US/10/741600
 Publication No. US20050026169A1

GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1396
 LENGTH: 388
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1396

Query Match 50.6%; Score 1042.5; DB 5; Length 388;
 Best Local Similarity 72.2%; Pred. No. 3.5e-77; Gaps 1;
 Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MAQWDDPPDQOEDTDSCTESVFKDARAVTALLPPHPKNGPQLQERMSKSYKALITYLIV 60
 Db 1 MEQWDDPPDQOEDTDSCTESVFKDARAVTALLPPHPKNGPQLQERMSKSYKALITYLIV 60

Qy 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119
 Db 61 FVVLVLTIGVAAQLKWTCTVSVA-DISPPEKGKNGSDEMRFREAVMRMSN 119

Qy 120 MERSICQLSDNBANLDAKNPONFSTTIDQRENDFVPLQNSLSSQBHENIGTIDISKSL 179
 Db 120 MERSICQLSDNBANLDAKNPONFSTTIDQRENDFVPLQNSLSSQBHENIGTIDISKSL 179

Qy 121 MEKRICHILDMEANTLMDTERFQNPFSMTDQRENDFLQLSTLFSVQGHNADEISKSL 180
 Db 121 MEKRICHILDMEANTLMDTERFQNPFSMTDQRENDFLQLSTLFSVQGHNADEISKSL 180

APPLICANT: Isaacs, William B.

APPLICANT: Blecker, Eugene

TITLE OF INVENTION: MUTATIONS IN THE MACROPHAGE SCAVENGER RECEPTOR 1 GENE ALTER RISK

TITLE OF INVENTION: OF PROSTATE CANCER, ASTHMA, AND CARDIOVASCULAR DISEASE

FILE REFERENCE: 9151-23

CURRENT APPLICATION NUMBER: US/10/426,262

CURRENT FILING DATE: 2003-05-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.2

SEQ ID NO: 2

LENGTH: 451

TYPE: PRT

ORGANISM: Homo sapiens

US-10-426-262-2

Query Match 50.6%; Score 1042.5; DB 4; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

Query Match 50.6%; Score 1042.5; DB 3; Length 451; Best Local Similarity 72.2%; Pred. No. 4.3e-77; Mismatches 197; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

Matches 137; Conservative 41; MisMatches 34; Indels 1; Gaps 1;

US-09-909-743-10

PRIOR APPLICATION NUMBER: US 60/248,325
 PRIOR FILING DATE: 2000-11-14
 PRIOR APPLICATION NUMBER: US 10/003,690
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/248,893
 PRIOR FILING DATE: 2000-11-15
 PRIOR APPLICATION NUMBER: US 09/797,039
 PRIOR FILING DATE: 2001-02-28
 PRIOR APPLICATION NUMBER: US 60/186,061
 PRIOR FILING DATE: 2000-02-29
 PRIOR APPLICATION NUMBER: US 10/217,168
 PRIOR FILING DATE: 2002-08-12
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 119
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 80
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-423-543-80

Query Match 50.6%; Score 1042.5; DB 4; Length 451;

Best Local Similarity 72.2%; Pred. No. 4.3e-77; Matches 197; Conservative 41; Mismatches 34; Index 1; Gaps 1;

Qy 1 MAQWDDDPDQOBDDTSCSTESKFDARSVTALLPPHRKGPTLQERMKSYKTAITYLIV 60
 Db 1 MEQWDRFHNOQBDTSCSESTKFDARSMTALLPPPKNSPSLOEKIKSKFKAIALYLV 60
 Qy 61 FVVLVLTIGIVAAQLKWTCKTGVSYNA-DISPPGKNGSSEDEMFRFRAVEMRSN 119
 Db 61 FAVLVLPLIGIVAAQLKWTCKTGVSYNA-DISPPGKNGSSEDEMFRFRAVEMRSN 120
 Qy 120 MESRQYLSDEANUAKQFQNSITDQRFDVLFQQLSSQIHEHNIIGISKL 179
 Db 121 MEKRQHILDEANUAKQFQNSITDQRFDVLFQQLSSQIHEHNIIGISKL 180
 Qy 180 VGLNTVLDIQLPSIETLNGRQENAPKQEMKLERIYMASBTKSLDEKQVYQLEI 239
 Db 181 ISLNTLILQDQNIENNGKQENTPKQEBISKLERIVNVSAEIMAKKEQVHLEI 240
 Qy 240 KGEKMKLANNITNDLRKDWEHSQTLRNTLQG 272
 Db 241 KGEVKVVLANNITNDLRKDWEHSQTLRNTLQG 273

RESULT 11

US-0-805-018-19

Sequence 19, Application US/10800018
 Publication No. US20040176296A1
 GENERAL INFORMATION:

APPLICANT: Khadadoust, Mehran M.
 APPLICANT: MacBath, Kyle J.
 APPLICANT: Busfield, Samantha J.
 APPLICANT: McCarthy, Sean A.
 APPLICANT: Holtzman, Douglas A.
 APPLICANT: Gu, Wei
 APPLICANT: White, David
 APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL ITALY LOR-2, STRIFE, TRASH, BDSF, LRG, AND TITLE OF INVENTION: STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/805,018
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1195
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-423-543-80

RESULT 12

US-10-741-600-1395

Sequence 1395, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:

APPLICANT: CARGIL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 1195
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1395

Query Match 50.6%; Score 1042.5; DB 5; Length 451;

Best Local Similarity 72.2%; Pred. No. 4.3e-77; Matches 197; Conservative 41; Mismatches 34; Index 1; Gaps 1;

Qy 1 MAQWDDDPDQOBDDTSCSTESKFDARSVTALLPPHRKGPTLQERMKSYKTAITYLIV 60
 Db 1 MEQWDRFHNOQBDTSCSESTKFDARSMTALLPPPKNSPSLOEKIKSKFKAIALYLV 60

PRIOR APPLICATION NUMBER: 60/117,580
 PRIOR FILING DATE: 1999-01-27
 PRIOR APPLICATION NUMBER: 09/014,195
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/014,348
 PRIOR FILING DATE: 1998-01-27
 PRIOR APPLICATION NUMBER: 09/086,892
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 09/286,208
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 09/063,950
 PRIOR FILING DATE: 1998-04-21
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 176
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 19
 LENGTH: 451
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-806-018-19

RESULT 13
US-10-496-905-481
; Sequence 481, Application US/10496905
; Publication No. US20050192215A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J
; APPLICANT: Boyle, Bryan J
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUC
; FILE REFERENCE: HIS-BCIP/US
; CURRENT APPLICATION: US/10/496,905
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: PCT/US00/34263
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/04098
; PRIOR FILING DATE: 2001-02-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 481
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-496-905-481

Query Match 38.9%; Score 801; DB 5; Length 454;
Best Local Similarity 59.4%; Pred. No. 3.4e-57; Mismatches 158; Conservative 46; Indels 2; Gaps 2;

Qy 8 PDDQEDTDSCTESVKDARSTVALLPPPKGPTQERMYSKTYLITLIVFLVLPPI 67
Qy 9 PHEREDADCSSESVKDARSTVALLPPPKGPTQERMYSKTYLITLIVFLVLPV 68

Db 68 IGVIAQQLKETKNTGVS-NADISPSBEGKGNSEDMRFRAAMERMSNRSIQY 126

Db 69 VGIIVTAQQLANWEMCNCLVGSRNTSDTSQPMKENTSIVEMRF-TIMAHMKDMEERIQS 127
Db 70 FAVLPLIGIVAQQLKWTETNCVSSTNANDITOSLTKGNDSEEMPQEVMHNSN 120
Db 120 MESRTOYLSDEANLILDAKQEQNFSITDORFNDLFLQINSLLSASIQEHENNIGDISKL 179
Db 121 NEKRQOHILDEMEANLMDTEHQNFMSITDORFNDLFLQINSLLSASIQEHENNIGDISKL 180
Qy 180 VGLNTVFLQFQSITETNGRVOENAPKQOEMRKLERTINASABIKSLDEKQYLEQEI 239
Db 181 ISLNNTFLDQIQLNIEINGKIQENTPKQOBISKLKEERVYKVSABEVNSABIMKBEQVHLQEI 240
Qy 240 KGEVKVLLNNTNDLRKDWEHQSTQTKNITLQG 272
Db 241 KGEVKVLLNNTNDLRKDWEHQSTQTKNITLQG 273

RESULT 14
US-09-782-980-126
; Sequence 126, Application US/09782980
; Patent No. US20020072089A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran M.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Busfield, Samantha J.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gu, Wei
; APPLICANT: White, David
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSC, AND
; TITLE OF INVENTION: STMS7 PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNT-121CP
; CURRENT APPLICATION NUMBER: US/09/782,980
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: PCT/US00/02125
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/448,076
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 09/276,400
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: 60/117,580
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 09/014,195
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/014,348
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/086,892
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/296,208
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 0/063,950
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 09/561,381
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,810
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 0/087,121
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/672,721
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/049,799
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 126
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-09-782-980-126

Query Match 38.9%; Score 801; DB 3; Length 458;
Best Local Similarity 59.4%; Pred. No. 3.5e-57; Mismatches 158; Conservative 46; Indels 60; Gaps 2;

QY 8 PPDQEQDTSCTESVKEDARSVTALLPPHPKGPTLQERMKSYKTAITLTYLIVVVLVPI 67
 ; :
 ; PHEREDADCSSESSEVKEDARSNTASLPHSTRKNGPSVQEKLKSFKAALIALYLVFAVLIPV 72
 Db 13 PHEREDADCSSESSEVKEDARSNTASLPHSTRKNGPSVQEKLKSFKAALIALYLVFAVLIPV 72
 QY 69 IGVIAQQLKMETKNTCTVGSN-ADSPSPRGKGNSEDENRFAEMEENNSMSRIOY 126
 ; :
 ; 73 VGIUTQQLNEMKNCVCSRNTSDTSQGPMEKENTSVNENRF-TIMAHMKDMERIOS 131
 Db 131 IGVIAQQLKMETKNTCTVGSN-ADSPSPRGKGNSEDENRFAEMEENNSMSRIOY 126
 QY 127 LSDNEANLDAKNFQNSITTDQRFNDVLFQNLNSLSSIQEHENIGDISKSLVGLANTV 186
 ; :
 ; 132 ISNSKADLIDGRFONFSMADQRANDILQNLNSLSSVQHGNSLDAISLSQNLMTL 191
 Db 132 ISNSKADLIDGRFONFSMADQRANDILQNLNSLSSVQHGNSLDAISLSQNLMTL 191
 QY 187 LDLOFSETLNGVRQENAFQKOBEMRKLBERIYNAEIKSLDENQVYLBQIKGEMKLL 246
 ; :
 ; 192 LDVOLHETELAVVRRESTAKOEDISKLEERVKYKSAEVQSVKEOAHVEQEVKOEVRVL 251
 QY 247 NNITNDLRLKOMEHSDQTLKNTLQG 272
 ; :
 Db 252 NNITNDLRLKOMEHSDQTLKNTLQG 277

RESULT 15
 US-10-806-018-126
 ; Sequence 126, Application US/10806018

PUBLICATION NO. US20040176296A1

GENERAL INFORMATION:
 ; APPLICANT: Khodadoust, Mehran M.

; APPLICANT: MacBeth, Kyle J.

; APPLICANT: Busfield, Samantha J.

; APPLICANT: McCarthy, Sean A.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Gu, Wei

; APPLICANT: White, David

APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL ITALY, LOR-2, SCRIBE, TRASH, BOSF, IRSG, AND

TITLE OF INVENTION: SIMT PROTEIN AND NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

CURRENT APPLICATION NUMBER: US/10/806, 018

CURRENT FILING DATE: 2004-03-22

PRIOR APPLICATION NUMBER: US/09/782, 980

PRIOR FILING DATE: 2001-02-13

PRIOR APPLICATION NUMBER: PCT/US00/02125

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 09/449, 076

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: 09/275, 400

PRIOR FILING DATE: 1999-03-25

PRIOR APPLICATION NUMBER: 60/117, 580

PRIOR FILING DATE: 1999-01-27

PRIOR APPLICATION NUMBER: 09/014, 195

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: 09/014, 348

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: 09/085, 892

PRIOR FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: 09/295, 208

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 09/063, 950

PRIOR FILING DATE: 1998-04-21

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 176

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 126

LENGTH: 458

TYPE: PRT

*ORGANISM: Mus musculus

US-10-806-018-126

Search completed: February 16, 2006, 17:09:31
 Job time : 167 secs

QY 8 PPDQEQDTSCTESVKEDARSVTALLPPHPKGPTLQERMKSYKTAITLTYLIVVVLVPI 67
 ; :
 ; PHEREDADCSSESSEVKEDARSNTASLPHSTRKNGPSVQEKLKSFKAALIALYLVFAVLIPV 72
 Db 13 PHEREDADCSSESSEVKEDARSNTASLPHSTRKNGPSVQEKLKSFKAALIALYLVFAVLIPV 72
 QY 68 IGVIAQQLKMETKNTCTVGSN-ADSPSPRGKGNSEDENRFAEMEENNSMSRIOY 126
 ; :
 ; 73 VGIUTQQLNEMKNCVCSRNTSDTSQGPMEKENTSVNENRF-TIMAHMKDMERIOS 131
 Db 131 IGVIAQQLKMETKNTCTVGSN-ADSPSPRGKGNSEDENRFAEMEENNSMSRIOY 126
 QY 127 LSDNEANLDAKNFQNSITTDQRFNDVLFQNLNSLSSIQEHENIGDISKSLVGLANTV 186
 ; :
 ; 132 ISNSKADLIDGRFONFSMADQRANDILQNLNSLSSVQHGNSLDAISLSQNLMTL 191
 Db 132 ISNSKADLIDGRFONFSMADQRANDILQNLNSLSSVQHGNSLDAISLSQNLMTL 191
 QY 187 LDLOFSETLNGVRQENAFQKOBEMRKLBERIYNAEIKSLDENQVYLBQIKGEMKLL 246
 ; :
 ; 192 LDVOLHETELAVVRRESTAKOEDISKLEERVKYKSAEVQSVKEOAHVEQEVKOEVRVL 251
 QY 247 NNITNDLRLKOMEHSDQTLKNTLQG 272
 ; :
 Db 252 NNITNDLRLKOMEHSDQTLKNTLQG 277

Query Match 38.9%; Score 801; DB 4; length 458;
 Best Local Similarity 59.4%; Pred. No. 3 5e-5;
 Mismatches 158; Conservative 46; Mismatches 60; Indels 2; Gaps 2;

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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;~Publication No. US20050272054A1
;~GENERAL INFORMATION:
;~APPLICANT: CARGILL, Michele et al.
;~TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;~TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;~FILE REFERENCE: CL001559
;~CURRENT APPLICATION NUMBER: US/10/995, 561
;~CURRENT FILING DATE: 2004-11-24
;~NUMBER OF SEQ ID NOS: 85702
;~SOFTWARE: FastSEQ for Windows Version 4.0
;~SEQ ID NO: 888
;~LENGTH: 358
;~TYPE: PRT
;~ORGANISM: Homo sapiens
;~US-10-995-561-888
Query Match 50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
RESULT 3
US-10-995-561-889
; Sequence 889, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995, 561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 887
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-887
Query Match 50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
RESULT 4
US-10-995-561-887
; Sequence 887, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995, 561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 887
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-887
Query Match 50.6%; Score 1042.5; DB 6; Length 388;
Best Local Similarity 72.2%; Pred. No. 9.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
RESULT 5
US-10-995-561-886
; Sequence 886, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995, 561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 886
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-886
Query Match 50.6%; Score 1042.5; DB 6; Length 358;
Best Local Similarity 72.2%; Pred. No. 8.9e-67;
Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;
RESULT 6
1 MAQWDDPQDQEDTSCTESKFDARSVTALLPPHKGNGPTLOERMKSYKTAITYLIV 60
1 MEQWDHFHNQEQDTSCTESKFDARSVTALLPPHKGNGPTLOERMKSYKTAITYLIV 60
180 VGLNTVLDLQFSIETLNGRVOENAQKQEMRKLERITYNASEIKSDEKQYLEQI 239
181 ISLNTLILQNLNENLNGKIQENTFKQOBISKEERVYNVSABIMAMKEQVHLEQI 240
240 KGEMKLLNNITNDLRKDMHQSQTLNITLQG 272
241 KGEVKVLLNNITNDLRKDMHQSQTLNITLQG 273
Db 120 MESRQYLSNEANLDAKNPONFSITDORFNDVLQFOLNSLSSIOEHENIGDISKL 179
Db 121 MEKRIQHILDEANLMDTSHFQNSMTTORENDLQLSTLFSVQGNIAIBISKL 180
Db 180 VGLNTVLDLQFSIETLNGRVOENAQKQEMRKLERITYNASEIKSDEKQYLEQI 239
Db 181 ISLNTLILQNLNENLNGKIQENTFKQOBISKEERVYNVSABIMAMKEQVHLEQI 240
Db 240 KGEMKLLNNITNDLRKDMHQSQTLNITLQG 272
Db 241 KGEVKVLLNNITNDLRKDMHQSQTLNITLQG 273

;

SEQ ID NO 886

;

LENGTH: 451

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

US-10-995-561-886

Query Match 50.6%; Score 1042.5; DB 6; Length 451;

Best Local Similarity 72.2%; Pred. No. 1.2e-66; Matches 197; Conservative 41; Mismatches 34; Indels 1; Gaps 1;

;

Db 1 NEQWDDPPDQBDTSCTESTKFDARSVTALPPHRKNGPTIQRERMKSYKTYALITYLIV 60

Qy 61 FVVLVLLIGIVAAQKXWETKNTGVSNA-DISPEPGKNGSEDEMFRERWMSN 119

Db 61 FAVLPLPLGIVAAQKXWETKNTGVSNTNANDITOSLTGKNDSEBEMFRERWMSN 120

Qy 120 MESRQYLSDEANUADAKNQNSITDQRFNDVIFQIANSLSQIQRERHIGDISL 179

Db 121 NEKRQHILDEHNEANLMDTEHNFNSMFDENFLQLOSLTSPSYQGHNAIDEKSL 180

Qy 180 VGLNTTVLDQSIETLNGRVQENAFAKQERKUBERIYNAESAETKSLDRQVYQEI 239

Db 181 ISLNNTLUDQIENJANGKIQENTFKQEQEISKLRSERVVINSAEIMAMKEEQVHUEQI 240

Qy 240 KGEMKMLANNTNDLQDWEISQTLNITLG 272

Db 241 KGEGVKVLUANTNDLQDWEISQTLNITLG 273

;

RESULT 6

US-10-673-781-1

;

Sequence 1, Application US/10673-781

;

Publication No. US20050260689A1

;

GENERAL INFORMATION:

;

APPLICANT: Qihwei Shi

;

TITLE OF INVENTION: Differential Immunoassay

;

FILE REFERENCE: 1112-1-080N

;

CURRENT APPLICATION NUMBER: US/10/673, 781

;

CURRENT FILING DATE: 2003-09-29

;

PRIOR APPLICATION NUMBER: US/09/938, 270B

;

PRIOR FILING DATE: 2001-08-23

;

PRIOR APPLICATION NUMBER: US 60/227, 536

;

PRIOR FILING DATE: 2000-08-24

;

PRIOR APPLICATION NUMBER: US 60/292, 497

;

PRIOR FILING DATE: 2001-05-21

;

NUMBER OF SEQ ID NOS: 2

;

SOFTWARE: FastSEQ for Windows Version 4.0

;

SEQ ID NO 1

;

LENGTH: 421

;

TYPE: PRT

;

ORGANISM: homosapien

;

US-10-673-781-1

;

RESULT 6

US-11-123-696A-3

;

Sequence 3, Application US/11123696A

;

Publication No. US2006024766A1

;

GENERAL INFORMATION:

;

APPLICANT: Atwell, John Leslie

;

APPLICANT: Devine, Peter Leonard

;

APPLICANT: Kortt, Alexander Andrew

;

APPLICANT: Perry, Julian Wendy

;

APPLICANT: Bundersen, Peter Gregory

;

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES

;

FILE REFERENCE: 674537-2001.1

;

CURRENT FILING DATE: 2005-05-05

;

PRIOR APPLICATION NUMBER: 09/581, 924

;

PRIOR FILING DATE: 2000-06-19

;

PRIOR APPLICATION NUMBER: PCT/AU98/01076

;

PRIOR FILING DATE: 1998-12-24

;

PRIOR APPLICATION NUMBER: AU PP1110

;

PRIOR FILING DATE: 1997-12-24

;

PRIOR APPLICATION NUMBER: AU PP5176

;

PRIOR FILING DATE: 1998-08-11

;

NUMBER OF SEQ ID NOS: 6

;

SOFTWARE: Patentin Ver. 3.3

;

SEQ ID NO 3

;

LENGTH: 270

;

TYPE: PRT

;

FEATURE:

;

ORGANISM: Artificial Sequence

;

OTHER INFORMATION: Description of Artificial Sequence

;

OTHER INFORMATION: construct of S. avidini and human immunoglobulin

;

US-11-123-696A-3

;

RESULT 8

US-10-878-556A-169

;

Sequence 169, Application US/10878556A

;

Publication No. US20050266399A1

;

GENERAL INFORMATION:

;

APPLICANT: Hoffmann La-Roche Inc.

;

TITLE OF INVENTION: HCV regulated protein expression

;

FILE REFERENCE: 21762

;

CURRENT APPLICATION NUMBER: US/10/878, 556A

;

CURRENT FILING DATE: 2004-06-28

;

NUMBER OF SEQ ID NOS: 199

;

SOFTWARE: Patentin version 3.1

;

SEQ ID NO 169

;

LENGTH: 1404

;

TYPE: PRT

;

ORGANISM: Homo sapiens

;

PUBLICATION INFORMATION:

;

DATABASE ACCESSION NUMBER: humanqp/chr12-q14221

;

DATABASE ENTRY DATE: 2003-04-22

;

US-10-878-556A-169

;

Query Match 6.7%; Score 138.5; DB 6; Length 421;

Best Local Similarity 33.1%; Pred. No. 0.0091; Matches 43; Conservative 18; Mismatches 56; Indels 13; Gaps 7;

;

Db 273 ARKCSLTGKWNLDGNSNTIGAVNSRGFTGTTAV-TATSNELIKSPLHGQTNTKRTQ 333

Qy 13 KABAGITGTGWNQLGSTIVAA-GADGALGTTGTESAVGNAESRYVLTGRTYDASAPATDGGT- 80

Db 23 EAGITGTTWYQLGSTIVAA-GADGALGTTGTESAVGNAESRYVLTGRTYDASAPATDGGT- 80

Qy 334 PTGGFTNWK---FSESTTIVFTGQCFIDRNGKEV-LKTMWLLRSSVNDGDKWTRVG 388

Db 81 -ALGWTAWKONYRNHAHSATWMSGQY---GGAEARINTQWLLTSGTE-ANAWKSTLVG 135

Qy 389 INIFTRUR 396

Db 136 HDTFIKVK 143

;

RESULT 7

;

Query Match 6.3%; Score 129; DB 6; Length 1404;

Best Local Similarity 21.5%; Pred. No. 0.21; Matches 98; Conservative 69; Mismatches 175; Indels 114; Gaps 18;

9 DQEDPDSCTESVKFDRSVTALLPPHPKNGPTLOEMRSYKTAITLTLYLIVFV 57

Db 671 DRQOEINKITD--QVTAQKQDQKQHQSOLSHKEYKYSLEQTEELRGQIK 726

Qy 58 -----LIVVPIGIVAAQLK-WETKNTGVSNTADSPSPEKGNSSEDEMPPREAV-- 97

Db 727 KLEADSLEVVKASKEQDLOQORQDNTDLRATLSKOLEMEKSVSTRBLQKSE 786

Qy 98 G----KGNSSEDEMPPREAVMRNSMNSRQYISDNEANLDDAKNFQNSITDQF 151

Db 835 QXVKMEKALMTTELSTVKDKUSKVSLSKNSKEFENOKKAALIDLEKICKELKHOL 894

Qy 787 ALESIKOKLTKEBEKKLKQFETLS-QETKLOH-----ERLNRIOTTTEL 834

Db 152 NDVLQFQLNSLASSIOHENITGDISKLQVGLNT-----TVIDLQSIETLNGRV 200

Qy 894 QXVKMEKALMTTELSTVKDKUSKVSLSKNSKEFENOKKAALIDLEKICKELKHOL 894

Db 201 Q----ENAPKQOEMRMLKURBERTYNASAK-----SLDEKQVYRQETKGEMKLLN 249

Qy 895 QVOMENTIKEQBLKLSLEKEKEASHQHKLNSMBOQHQNTLQNEKEBQOQQLN 954

Db 250 TNDLRLKQWERSQTLQKNTLQGARKSLSGK-WTNDLGSNTIGAVNSRGEFTQVIT 307

Qy 955 -NELKQSS--EOKKQOIEALOGELKIAVLOKTELENKQDQDLOTOAELAE----KE 1005

Db 1049 ISLAQEDLISRNQIGNONK-----LIOELKTAK 1077

RESULT 9 US-11-124-368A-214

; Sequence 214, Application US/11124368A.

Publication No. US2005028759A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: James J. Devlin

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with Title of Invention: Vascular Diseases, Methods of Detection and Uses Thereof

FILE REFERENCE: C1001524

PRIOR APPLICATION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-05-07

PRIOR APPLICATION NUMBER: US 60/625,936

PRIOR FILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 2112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 215

LENGTH: 2668

TYPE: PRT

ORGANISM: Homo sapiens

US-11-124-368A-215

Query Match 6.1%; Score 125.5; DB 7; length 2668;

Best Local Similarity 20.1%; Pred. No. 0.87%;

Matches 92; Conservative 90; Mismatches 157; Indels 119; Gaps 20;

Qy 3 QWDPPDQDQDPTDSCTESVKFDRSVTALLPPHPKNGPTLOEMRSYKTAITLTLYLIVFV 62

Db 888 EMEQLKQEQLERNDSTLQVEREKTLLTEKQOOLTEVKTLQEKDLQKQESL----- 941

LENGTH: 2665

TYPE: PRT

ORGANISM: Homo sapiens

US-11-124-368A-214

Query Match 6.1%; Score 125.5; DB 7; length 2665;

Best Local Similarity 20.1%; Pred. No. 0.87%;

Matches 92; Conservative 90; Mismatches 157; Indels 119; Gaps 20;

Qy 3 QWDPPDQDQDPTDSCTESVKFDRSVTALLPPHPKNGPTLOEMRSYKTAITLTLYLIVFV 62

Db 888 EMEQLKQEQLERNDSTLQVEREKTLLTEKQOOLTEVKTLQEKDLQKQESL----- 941

LENGTH: 2665

TYPE: PRT

ORGANISM: Homo sapiens

US-11-124-368A-214

Query Match 6.1%; Score 125.5; DB 7; length 2668;

Best Local Similarity 20.1%; Pred. No. 0.87%;

Matches 92; Conservative 90; Mismatches 157; Indels 119; Gaps 20;

Qy 63 VLVPIGIVAAQLKMETKNTGVSNTADSPSPEKGNSSEDEMPPREAV--MERMSN 119

Db 942 -----QIERDQLKSDHDNTWNMID-TOSOLRNALSLQHOEHTINTLKSISE 989

Qy 120 MERSIQQLSDNEANL-----DAKNFQNSITDQFNDVFLQNSLLS 163

Db 990 EVSRNLHMEETGETKDFQKMGIDKQDLEAKTO-TTADYKNELEQORKIFS 1047

Qy 164 SIOHENITGDISKLQVGL-----LNTVFLQFSL-TLING---RYOENAFQKQEE--- 210

Db 1048 LIQE-KNQLOMGEESTIAEKQQLK-----DIEGENIENTIENOELRILGDEKLKQOSVA 1103

Qy 211 -----MRKLEERYINASAEIKSDEKQVYQLEQIKGEMKLN--NI 249

Db 942 -----QIERDQLKSDHDNTWNMID-TQEQLNALSLQHOEHTINTLKSISE 989

Qy 120 MERSIQQLSDNEANL-----LDAKNFQNSITDQFNDVFLQNSLLS 163

Db 1104 ERNHA1KKEGELSRTCDRLLAEVEKLUKEKQSOLOQEQKQOLNQVQEMSEMOKKINETENL 1163

Qy 250 TNDLRLKD--WEHQSLQKNTLQGARKC-----SLT-GKWTDLGSNTIGAVNS 297

RESULT 11
US-10-793-636-2964
Sequence 2964, Application US/10793626
Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMELER, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIORITY APPLICATION NUMBER: 60/164, 258
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1660
LENGTH: 885
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-1660

Query Match 5.9%; Score 122.5; DB 6; Length 5024;
Best Local Similarity 21.5%; Pred. No. 3.3; Mismatches 153; Indels 111; Gaps 17;
Matches 90; Conservative 64; Mismatches 153; Indels 111; Gaps 17;

73 AQLKQWETKNTCTGVSNADISPSPECKGNCSDEMRPREAV----MERUNMSRSIQL 127
324 AKULK--AKEDAVASIN-NLS----GLTNEOKTKENQAVNGSQTRDQVANLRSKAL 374

128 SDNEANLDAKNFQNSITDQRFDVLFLNLSLSSIQHENI----GDISLVLG- 181
375 DO-NQTLRUVNNGVHIS-NSYFEDSTGKTYNAIDNGSTY-TGORNSELNSTID 434

182 ---LNTTVDL-----QFSIE--TLNG----RVQE-- 202
435 TISQINTAKNDLHGAEKLQRDGKTNQEQIGOLGYIANDPKSAEELVNGSNTRSEVEHL 494

203 -----NAPKQOESMRKLERIYMASBTKSLDKQKVYEBIGKGMKLNNTNDL 255
495 NEAKGLNNAMKOLRDKVAEKTNVKQSSDYINDSTHORGYDQALOBAENIINECNP-TL 553

256 KDWHEISQTLKNT-----LLQGARKCSLT-----GKWTNDLGSNMTI 292
554 NKSBEIQKQIQLTDQNALQGSHLLEAKONAITEENKLTALNDAMORQATENVQAOQTI 613

293 GAVNSRGEPTGTYTAVTATSNETI-KESPLUGTQNTINKRQOPTGFTVWKFSSSTTVF 351
614 PAVNOQTLDRREINTAMQALRDKVQONVWQOSNQYFNEDEQP-----KHNIDNSVQ 665

352 TQGCFIDR-----NGKEV-----LKTWMLRSVNDIGDWMKTRVGINFTLRT 397
666 AGQTTRIDKQDPPMIMKNEIQAQINTTQALSGENKLHDQESTNRQIEGLSSLNT 723

RESULT 12
US-10-793-626-1660
Sequence 1660, Application US/10793626
Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMELER, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIORITY APPLICATION NUMBER: 60/164, 258
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1660
LENGTH: 885
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-1660

Query Match 5.8%; Score 120; DB 6; Length 885;
Best Local Similarity 23.4%; Pred. No. 0.49; Mismatches 72; Indels 34; Gaps 7;
Matches 45; Conservative 41; Mismatches 72; Indels 34; Gaps 7;

97 EGKENGSDDEMRFREAVMRMSMSRSIQL---SDNEANLDAKNFQNSITDQREN 152
108 ERKGNQSETNARV-----BELLNLSQDTSKIKOKEAQNEKLLABELKLNKO----KQLN 156

153 DVLQFQNSL--S-SIQEHENIIGDLSKLSVLGANTVLDIQQSIEITNGVQEN----- 203
157 KEVOBLESLILYSDSDEQHDEKLEETKNSVYTLMSBOSDVNDIRFLEHTINNEAKSRD 216

204 -----AFKQ---QEBMRKLEERYNASBIAKSIDBKQVLEQIKGEMKLNNTDLR 254
Db 217 SRVLFAPNQKQDQONITQOTQEKVQSSKSKMSKEQNTQOLEQDLSKRLSEYENKL- 275

255 LKOWEHSHOTLN 266
Db 276 YQAVRYNERLKS 287

RESULT 13
US-11-152-697-2
Sequence 2, Application US/11152697
Publication No. US20060003367A1

GENERAL INFORMATION:
APPLICANT: BRISTOL-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN RUPPER CELL RECEPTOR
FILE REFERENCE: D0342_NP
CURRENT APPLICATION NUMBER: US/11/152, 697
CURRENT FILING DATE: 2005-06-14
PRIORITY APPLICATION NUMBER: 60/580, 006
PRIORITY FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 492
TYPE: PRT

ORGANISM: Homo sapiens
; US-11-152-697-2

Query Match 5.6%; Score 115.5; DB 7; Length 492;
Best Local Similarity 20.9%; Pred. No. 0.47; Mismatches 136; Indels 103; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

70 IVAQQLKQWETKNTCTGVSNADISPSPECKGNCSDEMRPREAVMERMSMSRSIQLSD 129
57 VWEIOMLK---CRVDDVNSQLOVIGLHGNNTAD-TWNVGVYDATTLSLOTOMLRS 110

130 NEANLDAKNFQNSITDQRFDVL-FQ-LNSLSSIQHENIIGDLSKLSVLGANTV 187

QY 339 TV-NWKFS 345
Db 468 MVLDQWKFEN 476

RESULT 15
US-10-793-626-3154
Sequence 3154, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164, 258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3154
LENGTH: 1095
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-3154

Query Match 5.4%; Score 110.5; DB 6; Length 1095;
Best Local Similarity 20.8%; Pred. No. 3.1; Gaps 14;
Matches 71; Conservative 59; Mismatches 125; Indels 87; Gaps 14;

QY 111 BAVMRMMNNESRIQYOLSDNEANLIDAKRQFQNFSTI-TDQRENDVLFQLNSSL 162
Db 469 BAVQKVNDAIHMLQKNNSA-LVTAKNOLQQVNDQPLTTGMQDPSINNYVAKRNEAQ 527

QY 163 SSIQHENNI-GD-ISSKSLVGLAN-TTFLDLOPSIETANGRVO 201
Db 528 SAIKNAEAVINVNGDATAKQISDEKSVEQALAHNDAKQQLTADTBLQAVQOLNRRGD 587

QY 202 ENAFKQO-EEMRKLEERITNARISRIKSLBEKQVYLEIKEGKMLNNITNDL- 253
Db 588 TNKKCPRSNAYNKAQIOLSTQITSAKDNANAVIKPRTVQVBNALQVQVNLQOLTE 647

QY 254 ---RJKDWEHSQTIK-NITLLOGARKCSLTGKWTNDLGS 288
Db 648 AINQLOPLSINNDALKGARUNLENKINQVOTDGMWQOSTEAYQAKRVA---QNE-S 700

QY 289 NMTCGAVNSKGFBFTYITAVTATNEIKESPLHG-TQNTINKRQOPTGFTVWKPS EST 348
Db 701 NTALALINN-GDADBQQITETDRVN-OQTN-LTOQINGLTVNKEPLE- 746

QY 349 TVFTGQCFDRNGKEVLTWMLRSSVNDGDKWATRGIN 390
Db 747 ---TAKTALQNNIDQVPSIDGMTOQSVANYNQKQIAQNBIN 785

RESULT 14

US-11-152-697-5

Sequence 5, Application US/11152697

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFER CELL RECEPTOR
TITLE OF INVENTION: PROTEIN, BGS-18
FILE REFERENCE: D0242 NP

CURRENT APPLICATION NUMBER: US/11/152,697

CURRENT FILING DATE: 2005-06-14

PRIOR APPLICATION NUMBER: 60/580,006

PRIOR FILING DATE: 2004-06-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PatentIn version 3.2

SEQ ID NO 5

LENGTH: 539

TYPE: PRT

ORGANISM: Homo sapiens

US-11-152-697-5

Query Match 5.6%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;

Query Match 7.0%; Score 115.5; DB 7; Length 539;

Best Local Similarity 20.9%; Pred. No. 0.53; Gaps 14;
Matches 77; Conservative 53; Mismatches 136; Indels 103; Gaps 14;Search completed: February 16, 2006, 17:09:55
Job time : 20 secs